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Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 1

CTAAAAAAATATGTTCTCTACAACACCAAGGCTCATTAATATTAAATATT  
AATATAACATTCTTCTGTCAGAAATACATAAAACTTATTATATCAGCGCAGG  
GCGGCGCGCGTCGGTCCCAGGAGCAGAACCCGGCTTTCTGGAGCGACG  
CTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTGCTACACTCTA  
ATCTGCGCAAACCTTGCAGCTGTCGGGACACTCTGCAACCCCCGAGAGCG  
CATCCATCAAAGCTTGCAGCACGCCAACCTCAGGCGAGATGAGAGCAATCA  
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGG  
CTACGTGCAGAGTCCTAGATTCCGAACAGCTACCCAGGAACCTGCTCCTG  
ACATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGACA  
ATCAGTTGGATTAGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTGT  
GGAAGTTGAAGATATATCGAAACCAAGTACCTATTAGAGGACATGGTGT  
GGACACAAGGAAGTCCCTCCAAGGATAAAATCAAGAACGAACCAAATTAAA  
ATCACATTCAAGTCCGATGACTACTTGTGGCTAACCTGGATTCAAGATTAA  
TTATTCTTGCTGGAAGATTCCAACCCCGCAGCAGCTCAGAGACCAACTGGG  
AATCTGTACAAGCTCTATTCAAGGCTATCTCAATCCAGAGTCATGGCAAGAACAT  
GATCCCACTCTGATTGCGGATGCTCTGGACAAAAAAATTGCAAGATTGATA  
CAGTGGAAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAACAT  
TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTACATACCATGAC  
CGGAAGTCAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACA  
GTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAACAGAGCTGAAGTTGGC  
CAATGTGGTCTTCTTCCACGTTGCCTCGTGCAGCGCTGTGGAGGAAATT  
GTGGCTGTGGAAGTGTCAACTGGAGGTCTGCACATGCAATTCAAGGAAAC  
CGTAAAAAGTATCATGAGGTATTACAGTTGAGCCTGGCACATCAAGAGG  
AGGGGTAGAGCTAACGACCATGGCTCTAGTTGACATCCAGTTGGATCACCATG  
AACGATGTGATTGTATCTGCAAGACCACTCGATAAGAGAACATGTGCA  
CATCCTACATTAAGCCTGAAAGAACCTTAGTTAAGGAGGGTGAGATAAG  
AGACCCCTTCTACCAGCAACCAAACCTACTAGCCTGCAATGCAATGA  
ACACAAGTGGTTGCTGAGTCTCAGCCTGCTTGTAAATGCCATGGCAAGTAG  
AAAGGTATATCATCAACTCTACACCAAGAATATAGGATTGCATTAAATAAT  
AGTGTGAGGTTATATATGCACAAACACACACAGAAATATATTGATGTCTAT  
GTGTATATAGATCAAATGTTTTGGTATATATAACCAGGTACACCAGAGC  
TTACATATGTTGAGTTAGACTCTTAAATCCTTGCCAAAATAAGGGATGGT  
CAAATATATGAAACATGTCTTAGAAAATTAGGAGATAAAATTATTTTAAA  
TTTGAAACACAAAACAATTGAAATCTGCTCTAAAGAAAGCATCTTGT  
ATATTAAAAATCAAAAGATGAGGCTTCTTACATATACATCTTAGTTG (SEQ  
ID NO:50)



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Figure 2A

1 CTAACAAATATGTTCTCTACAACACCAAGGCTCATTAACAAATTT  
46 TAAATATTAATATACTATTTCTCTGTCAAGAAATACATAAAACTTT  
91 ATTATATCAGCGCAGGGCGGCAGCGTCGGTCCCAGGAGCAGAA  
136 CCCGGCTTTCTTGAGCGACGCTGTCTCTAGCGCTGATCCCA  
  
181 AATGCACCGGCTCATCTTGCTACACTCTAAATCTGGCAAACCTT  
Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe  
10 226 TTGCAGCTGTCGGGACACTTCTGCAACCCCCGAGGCCATCCAT  
Cys Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile  
  
271 CAAAGCTTGCGAACGCCAACCTCAGGGAGATGAGAGCAATCA  
Lys Ala Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His  
15  
  
316 CCTCACAGACTTGTACCGAAGAGATGAGACCATTCCAGGTGAAAGG  
Leu Thr Asp Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly  
  
361 AACGGCTACGTGCAGAGTCTTAGATTCCGAACAGCTACCCAG  
Asn Gly Tyr Val Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg  
20  
  
406 GAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAATACAG  
Asn Leu Leu Leu Thr Trp Arg Leu His Ser Gln Glu Asn Thr Arg  
25  
  
451 GATACAGCTAGTGTGTTGACAATCAGTTGGATTAGAGGAAGCAGA  
Ile Gln Leu Val Phe Asp Asn Gln Phe Gly Leu Glu Glu Ala Glu  
  
496 AAATGATATCTGTAGGTATGATTGTGGAAAGTTGAAGATAATAC  
Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Asp Ile Ser  
30  
  
541 CGAAACCAAGTACCAATTATTAGAGGACGATGGTGTGGACACAAGGA  
Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly His Lys Glu  
  
586 AGTTCCCAAGGATAAAATCAAGAACGAAACCAATTAAATCAC  
Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys Ile Thr  
35  
  
631 ATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGAT



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PheLysSerAspAspTyrPheValAlaLysProGlyPheLysIle

**Figure 2B**

5            676 TTATTATTCTTGCTGGAAAGATTTCCAACCCGCAAGCAGCTTCAGA  
TyrTyrSerLeuLeuGluAspPheGlnProAlaAlaAlaSerGlu

10          721 GACCAACTGGGAATCTGTACAGCTCTATTTCAGGGTATCCTA  
ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr

15          766 TAACTCTCCATCAGTAACGGATCCCACCTCTGATTGCGGATGCTCT  
AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu

20          811 GGACAAAAAAATTGCAGAAATTGATAACAGTGGAAAGATCTGCTCAA  
AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys

25          856 GTACTTCAAATCCAGAGTCATGCCAAGAAGATCTTGAGAAATATGTA  
TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr

30          901 TCTGGACACCCCCCTGGTATCGAGGCAGGTCATACCAGACCCGAA  
LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys

35          946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAACCGTTA  
SerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyr

40          991 CAGTTGCACCTCCAGGAATTACTCGGTCAATATAAGAGAACAGCT  
SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu

45          1036 GAAGTTGGCCAATGTGGCTTCTTCCACGTTGCCCTCTCGTGC  
LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln

50          1081 GCGCTGTGGAGGAAATTGTGGCTGTGGAACTGTCAACTGGAGGTC  
ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer

55          1126 CTGCACATGCAATTCAAGGGAAAACCGTGAAAAAGTATCATGAGGT  
CysThrCysAsnSerGlyLysThrValLysLysTyrHisGluVal

60          1171 ATTACAGTTGAGCCTGGCCACATCAAGAGGGAGGGTAGAGCTAA  
LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys



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1216 GACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATG  
ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys

5 1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAAGAGAAATGTGCA  
AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)

10 1306 CATCCTTACATTAAGCCTGAAAGAACCTTTAGTTAAGGAGGGTG  
1351 AGATAAGAGACCCTTTCTACCAAGCAACCAAACCTACTACTAGC  
1396 CTGCAATGCAATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCT  
1441 TTGTTAATGCCATGGCAAGTAGAAAGGTATATCATCAACTTCTAT  
1486 ACCTAAGAATATAGGATTGCATTTAATAATAGTGTGAGGTTAT  
1531 ATATGCACAAACACACACAGAAAATATTCATGTCTATGTGTATA  
1576 TAGATCAAATGTTTTTTGGTATATATAACCAGGTACACCAGAG  
1621 CTTACATATGTTGAGTTAGACTCTAAATCCTTGCCAAAATA  
1666 AGGGATGGTCAAATATATGAAACATGTCTTTAGAAAATTTAGGAG  
1711 ATAAATTTATTTTAAATTTGAAAACACAAAACAATTGAAATCT  
1756 TGCTCTCTAAAGAAAGCATCTGTATATTAAAAATCAAAAGATG  
1801 AGGCTTTCTTACATATACATCTTAGTTG (SEQ ID NO:50)

Figure 2C



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**FIGURE 3**

A -- Cur2 1.6 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGTCCC  
TGAGACTCTCCTGTGCAGCCTCTGGATTCAACTTCAGAACCTATAACATGAAC  
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTA  
GTAGTAGTAGTAACATATACTACGCAGACTCAGTGAAGGGCCGATTCAACCCT  
CTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTATATTACTGTGCGAGAGATATTATGATTACGTTG  
GGGAATTATCGCCTCGTTCTACTTGACTACTGGGCCAGGGAACCCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

EVQLVESGGGLVKPGGSLRLSCAASGFNFRTYNMNWVRQAPGKGLEWVSSISSS  
SSNIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIAS  
FYFDYWQGTLTVSS (SEQ ID NO:13)

C -- Cur2 1.6 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TTTCAGCAGAAACCAGGGAAAGCCCCCTAACGGCCTGATCTATGCTGCATCCA  
GTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCGCTACTTCGGCGGAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:56)

D -- Cur2 1.6 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWFQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKEIK (SEQ  
ID NO:14)



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**FIGURE 4**

A -- Cur2 1.11 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCTGGAGGAGGCTTGATCCAGCCTGGGGGGTCCC  
TGAGACTCTCCTGTGCAGCCTCTGGGTTCACCGTCAGTAGCAACTACATGAGC  
TGGGTCCGCCAGGCTCCAGGGAAAGGGGCTGGAGTGGGTCTCAGTTATTATA  
GCGGTGGTAGCACATACTACCGCAGACTCCGTGAAGGGCCGATTCACCATCTC  
CAGAGACAATTCCAAGAACACCGCTGTATCTCAAATGAACAGCCTGAGAGCC  
GAGGACACGGCCGTGTATTACTGTGCAGGAAACGGTACTACGAATTACTACT  
ACGGTATGGACGTCTGGGCAAGGGACCACGGTCACCGTCTCCTCAG (SEQ  
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

EVQLVQSGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSG  
GSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTNYYGM  
DVWGQGTTVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC  
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCTGCAAAGTAATGGATAC  
AACTATTGGATTGGTACCTGCAGAACCCAGGGCAGTCTCACAGCTCCTGA  
TCTATTGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTCAGTGGCAGT  
GGATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG  
TTGGGGTTATTACTGCATGCAAGCTCTACAAACTCTCACTTCGGCGGAGGG  
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLLQSNGNYLDWYLQKPGQSPQLLIYLG  
SNRASGPDRFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTLFGGGTKVEI  
K (SEQ ID NO:16)



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**FIGURE 5**

A -- Cur2 1.17 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCC  
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC  
TGGGTCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGT  
ATGATGGAAGTAATAAACTATGCAGACTCCGTGAAGGGCCGATTACCAT  
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAACAGCCTGAGA  
GCCGAGGGACACGGCTGTGTATTACTGTGCGAGAGATCAAGGATACAGATATG  
CTGGTTACTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:59)

B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW  
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYA  
GYYYDYGMDVWQGQGTTVTVSS (SEQ ID NO:17)

C -- Cur2 1.17 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCATAAGCGCCTGATCTATGCTGCATCCA  
GTTTGCAAAGTGGGGTCCCCTCAAGGTTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTCGAACCTATTACT  
GTCTACAGCATAATAGTTACCCGCTACTTCGGCGGAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:60)

D -- Cur2 1.17 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKEIK (SEQ  
ID NO:18)



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**FIGURE 6**

A -- Cur2 1.18 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTCACCAAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCAAACAGTGGTAACACAGGCTATGCACAGAACAGTTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCGTGTATTACTGTGCGAGAGAGGGTATAGCAGTGGC  
TGGGACATACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG  
GTCACCGTCTCCTCAG (SEQ ID NO:61)

B -- Cur2 1.18 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAG  
YYYYYYGMDVWGQGTTVTVSS (SEQ D NO:19)

C -- Cur2 1.18 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAACAGGTTAGCAGCGCCTGATCTATGCTGCATCCA  
GTTTGCAAAGTGGGGTCCCCTAACAGGTTAGCAGCGCAGTGGATCTGGGACAGA  
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTCT  
GTCTACAGCATAATAGTTACCCATTCACTTCGGCCCTGGGACCAAAGTGGAT  
ATCAAAC (SEQ ID NO:62)

D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ  
ID NO:20)



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**FIGURE 7**

A -- Cur2 1.19 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC  
TGGGTGCACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAAC  
CCTAACAGTGGTAACACACAGGCTATGCACAGAAAGTTCCAGGGCAGAGTCACCA  
TGACCAGGAACACCTCCATAAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG  
ATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTG  
GGGGAGTTATCGTGCACTACGGTATGGACGTCTGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:63)

B -- Cur2 1.19 heavy chain amino acid sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFG  
GVIVHYGMDVWGQGTTVTVSS (SEQ ID NO:21)

C -- Cur2 1.19 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAACGCGCCTGATCTATGCTGCATCCA  
GTTTGCAAAGTGGGGTCCCCTAACGGTTAGCGGGCAGTGGATCTGGGACAGA  
TTTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTGACCCGTGCAGTTGGCCAGGGACCAAGCTGGA  
GATCAGAC (SEQ ID NO:64)

D -- Cur2 1.19 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKR<sup>L</sup>IYAASSLQ  
SGVPSRFSGS<sup>G</sup>TDFLTISLQPEDFATYYCLQHNSDPCSFGQGT<sup>K</sup>LEIR (SEQ  
ID NO:22)



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**FIGURE 8**

**A -- Cur2 1.23 heavy chain nucleotide sequence**

```
GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGAGTCT  
CTGAAGATCTCCTGTGAGGGTTCTGGATACAGCTTACCAAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTGACTCTGATACCAGATAACAGCCCCTCCCAAGGCCAGGTACCCA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCAGACATGTATCGTATTACTATG  
TTTCGGGGAGTTATTATAACGTCTTGACTACTGGGCCAGGGAACCCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:65)
```

**B -- Cur2 1.23 heavy chain amino acid sequence**

```
EVQLVQSGAEVKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDTRYSPSFQGVVTISADKSISTAYLQWSSLKASDTAMYCARHVSYYYVSGS  
YYNVFDYWQQGTLTVSS (SEQ ID NO:23)
```

**C -- Cur2 1.23 light chain nucleotide sequence**

```
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGATACCAGGGAAAGCCCCTAACGCGCCTGATCTATGCTGCATCCA  
GTTTGCACACGTGGGGTCCCCTAACAGGTTCAAGCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTCGAACCTATTACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:66)
```

**D -- Cur2 1.23 light chain amino acid sequence**

```
DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQIPGKAPKRLIYAASSLQR  
GVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:24)
```



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**FIGURE 9**

A -- Cur2 1.24.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC  
TGAGACTCTCCTGTGCAGCGTCTGGATTCACTTCAGTAGCTATGGCATGCAC  
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGT  
ATGATGGAAGTAATAAAATACTATGCAGACTCCGTGAAGGGCCGATTACCAT  
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGGACACGGCTGTGTATTATTGTGCGAGAGATCAGGGATAACAGCTATG  
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:67)

B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIW  
YDGSNKYYADSVKGRTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYSYG  
YVYYDYGMDVWGQGTTVTVSS (SEQ ID NO:25)

C -- Cur2 1.24.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAAATGATTTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGGCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTTCAAAGTGGGGTCCCCTCAAGGTTCAGCGGCAGTGGATCTGGGACAGA  
GTTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:68)

D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:26)



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**FIGURE 10**

A -- Cur2 1.25.1 heavy chain nucleotide sequence

```
GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCAGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTCTGGATACAGGTTACCAGCTACTGGATCGG  
CTGGGTGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTGAECTGATACAGATAACAGCCCCTACCTGCAGTGGAGCAGCCTGAA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTATTATG  
GTTCGGAGACTTATTATAATGTCTTGACTACTGGGCCAGGGAACCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:69)
```

B -- Cur2 1.25.1 heavy chain protein sequence

```
EVQLVQSGAEVKPGESLKISCKGSYRFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDTRYSPSFQGVVTISADKSISTAYLQWSSLKASDTAMYCARHGSYYGSET  
YYNVFDYWQGQTLTVSS (SEQ ID NO:27)
```

C -- Cur2 1.25.1 light chain nucleotide sequence

```
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAACGGCCTGATCTATGCTGCATCCA  
GTTTGCAAAGTGGGGTCCCCTAACGGTTCAGCGGCAGTGGATCTGGACAGA  
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:70)
```

D -- Cur2 1.25.1 light chain protein sequence

```
DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:28)
```



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**FIGURE 11**

A -- Cur2 1.29 heavy chain nucleotide sequence

```
GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCAGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTCTGGATACAGCTTACCAAGCTACTGGATCGG  
CTGGGTGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTACTCTGATACCAGATAACAGCCCCTCCAAAGGCCAGGCCACCA  
TCTCAGCCGACAAGTCCATCAGCACCGCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACGTGGATGTAGGGCT  
ACGATTGGGGATATTACTATTACTACCACGGTATGGACGTCTGGGCCAAG  
GGACCACGGTCACCGTCTCAG (SEQ ID NO:71)
```

B -- Cur2 1.29 heavy chain protein sequence

```
EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDTRYSPSFQGQATISADKSISTAYLQWSSLKASDTAMYCARHVDVGATIGG  
YYYYYHGMDVWGQGTTVTVSS (SEQ ID NO:29)
```

C -- Cur2 1.29 light chain nucleotide sequence

```
GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC  
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCTGCATAGTAATGGATACA  
ACTATTGGATTGGTACCTGCAGAACGCCAGGGCAGTCTCCACAACCTCTGATC  
TATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTAGTGGCAGTGG  
ATCAGGCACAGATTTACACTGAAAATCAGCAGAGTGGAGGCTGACGATGTT  
GGGGTTTATTACTGCATGCAAGCTCTACAATCTCTCATGTGCAGTTGGCCA  
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)
```

D -- Cur2 1.29 light chain protein sequence

```
DIVMTQSPLSLPVTPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLIYLG  
SNRASGPDRFSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKL  
EIK (SEQ ID NO:30)
```



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**FIGURE 12**

A -- Cur2 1.33 heavy chain nucleotide sequence

CAGGTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTACCGCTATGGTATCAGC  
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCG  
CTTACAATGGTAACACAAACTATGCACAGAACGCTCCAGGGCAGAGTCACCAT  
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG  
ATCTGACGACACGGCCGTGTATTACTGTGCAGAGATCATTACTATGATAGT  
AGTGATTATCTCTACTACTACGGTTGGACGTCTGGGGCCAAGGGACCAC  
GGTCACCGTCTCCTCAG (SEQ ID NO:73)

B -- Cur2 1.33 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA  
YNGNTNYAQKLQGRVTMTTDSTSTAYMELRSLSRSDDTAVYYCARDHYDSS  
DYLYYYYGLDVWGQQTTVTVSS (SEQ ID NO:31)

C -- Cur2 1.33 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT  
ATCAGCAGAAACCAGGGAAAGTTCTAAGCTCCTGATCTATGCTGCATCCAC  
TTTGCATCAGGGTCCCATCTGGTTCACTGGCAGTGGATCTGGACAGATT  
TCACTCTCACCACATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTAACTGT  
CAAAGTATAACAGTGCCCGCTCACTTCGGCGAGGGACCAAGGTGGAGA  
TCAAAC (SEQ ID NO:74)

D -- Cur2 1.33 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQ  
SGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNNSAPLTFGGGTKVEIK (SEQ  
ID NO:32)



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**FIGURE 13**

**A -- Cur2 1.38.1 heavy chain nucleotide sequence**

CAGGTGCAGCTGGTGGAGTCGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC  
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC  
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGT  
ATGATGGAAATGATAAAACTATGCAGACTCCGTGAAGGGCCGCTTCACCGT  
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATTACTATGATAGTA  
GTGATTATCTCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC  
GGTCACCGTCTCCTCAG (SEQ ID NO:75)

**B -- Cur2 1.38.1 heavy chain protein sequence**

QVQLVESGGVVQPGRLSLSCAASGFTFSSYGMHWVRQAPGKGLEWVIAIWY  
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSS  
DYLYYYYYGMDVWGQGTTVTVSS (SEQ ID NO:33)

**C -- Cur2 1.38.1 light chain nucleotide sequence**

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCGAGTCAGGGCATTAGCAATTATTCAGCCTGGT  
ATCAGCAGAAACCAGGGAAAGTTCTAACCTCCTGATCTATGCTGCATCCAC  
TTTGCAATCAGGGGTCCCATCTCGGTTAGTGGCAGTGGATCTGGACAGATT  
TCTCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAGCTTATTACTGT  
CAAAAGTGTAAACAGTGCCCCGTGGACGTTGGCCAAGGGACCACGGTGGAG  
ATCAAAC (SEQ ID NO:76)

**D -- Cur2 1.38.1 light chain protein sequence**

DIQMTQSPSSLSASVGDRVITCRASQGISNYLAWYQQKPGKVPNLLIYAASTLQ  
SGVPSRFSGSGETDFSLTISSLQPEDVAAYYCQKCNSAPWTFGQGTTVEIK (SEQ  
ID NO:34)



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**FIGURE 14**

A -- Cur2 1.39.1 heavy chain nucleotide sequence

```
GAGGTGCAGCTGGTGCAGTCGGGAACAGAGGTGAAAAAGCCCAGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTGACTCTGATAACCAGATAACAGCCCCTACCTGCAGTGGAGCAGCCTGAA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTACTATA  
ATTCGGGGAGTTATTATAACGTCTTGAECTACTGGGCCAGGGAACCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:77)
```

B -- Cur2 1.39.1 heavy chain protein sequence

```
EVQLVQSGTEVKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDTRYSPSFQGVVTISADKSISTAYLQWSSLKASDTAMYCARHGSYYYNSGS  
YYNVFDYWGQGTLTVSS (SEQ ID NO:35)
```

C -- Cur2 1.39.1 light chain nucleotide sequence

```
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTTCAAAGTGGGGTCCCCTCAAGGTTAGCGGGAGTGGATCTGGGACAGA  
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:78)
```

D -- Cur2 1.39.1 light chain protein sequence

```
DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:36)
```



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**FIGURE 15**

A -- Cur2 1.40.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTACCACTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCCTAACGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT  
AGCTGCTACCAACTACTAACACGGTATGGACGTCTGGGGCCAAGGGACCACG  
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFYYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDTAVYYCARDIVVVV  
AATNYYNGMDVWGQGTTVTVSS (SEQ ID NO:37)



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**FIGURE 16**

**A -- Cur2 1.45 heavy chain nucleotide sequence**

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCAAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA  
TGGTTACGACTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTC  
ACCGTCTCCTCAG (SEQ ID NO:80)

**B -- Cur2 1.45 heavy chain protein sequence**

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYG  
YDYYYYGMDVWGQGTTVTVSS (SEQ ID NO:38)

**C -- Cur2 1.45 light chain nucleotide sequence**

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCAATTGCCGGCGAGTCAGGGCATTAGCAATGATTAGCCTGG  
TATCAGCAGAAACCAGGGAAAGTTCTAACAGCTCCTGATCTATGCTGCATCCA  
CTTGCAATTAGGGTCCCCTCTCGGTTAGTGGCAGTGGATCTGGACAGAT  
TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG  
TCAAAAGTATAACAGTGCCCCATTCACTTCGGCCCTGGGACCAAAGTGGAT  
ATCAAAC (SEQ ID NO:81)

**D -- Cur2 1.45 light chain protein sequence**

DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASTLQ  
LGVPSRFSGSQGTDFTLTISLQPEDVATYYCQKYNSAPFTFGPGTKVDIK (SEQ  
ID NO:39)



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**FIGURE 17**

A -- Cur2 1.46.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCCTCA  
GTGAAGGTCTCTGCAAGGCTCTGGATACTCCTCACCAAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCTAACAAATGGTAACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT  
AACTGCTACGGACTACTACCGGTATGGACGTCTGGGCCAAGGGACCACG  
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYSFTSYDINWVRQATGQGLEWMGWM  
NPNNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVT  
ATDYYYGMDVWGQGTTTVSS (SEQ ID NO:40)

C -- Cur2 1.46.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCATAAGCGCCTGATTTGCTGCATCCA  
GTTGCCAAGTGGGGTCCCCTCAAGGTTAGCGGGCAGTGGATCTGGACAGA  
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTATTACT  
GTCTACAGCATAGTGGTACCCCTCCGACGTTCGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:83)

D -- Cur2 1.46.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLPS  
GVPSRFSGSQSGTEFTLTISLQPEDFATYYCLQHSGYPPTFGQGTKVEIK (SEQ ID  
NO:41)



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**FIGURE 18**

**A -- Cur2 1.48.1 heavy chain nucleotide sequence**

CAGGTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTACCAGCTATGGTATCAGC  
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCG  
CTTACAATGGTAACACACAAACTATGCACAGAACAGCTCCAGGGCAGAGTCACCAT  
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG  
ATCTGACGACACGGCCGTATTACTGTGCGAGAGATGTTGAATATTACTATG  
ATGGTAGTGGTTATTACTACTTTGACTACTGGGCCAGGAAACCCTGGTCACC  
GTCTCCTCAG (SEQ ID NO:84)

**B -- Cur2 1.48.1 heavy chain protein sequence**

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA  
YNGNTNYAQKLQGRVTMTTDSTSTAYMELRSLSRSDDTAVYYCARDVEYYYD  
GSGYYYYFDYWGQGTLTVSS (SEQ ID NO:42)

**C -- Cur2 1.48.1 light chain nucleotide sequence**

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGTGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG  
TATCAGCAGAAACCAGGGAAAGGCCCTAACAGCTCTGATCTATGCTGCATCCA  
TTTGCAAAGTGGGGTCCCCTAACAGGTTAGCAGCGGAGTGGATCTGGGACAGA  
TTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATTTGCATCTTACTATT  
GTCAACAGTCTAACAGTTCCCTCGGACGTTGGCCAAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:85)

**D -- Cur2 1.48.1 light chain protein sequence**

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAA SILQ  
SGVPSRFSGSGTDFLTISLQPEDFASYYCQQSNSFPRTFGQGTKVEIK (SEQ  
ID NO:43)



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**FIGURE 19**

**A -- Cur2 1.49.1 heavy chain nucleotide sequence**

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA  
GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCAAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCTAACAGTGGTGACACAGGCTATGCACAGAACAGTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCGTGTATTCTGTGCGAGAATGAGGGATATAGTGGC  
TACGAGCTATTACTACTTCTACGGTATGGACGTCTGGGCAAGGGACC  
ACGGTCACCGTCTCCTCAG (SEQ ID NO:86)

**B -- Cur2 1.49.1 heavy chain protein sequence**

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARMRDIVAT  
YYYYFYGMDVWGQGTTVTVSS (SEQ ID NO:44)

**C -- Cur2 1.49.1 light chain nucleotide sequence**

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC  
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCTGCATAGTAATGGATACA  
ACTATTGGATTGGTACCTGCTGAAGCCAGGGCAGTCTCCACAGCTCCTGATC  
TATTGGGTTCTAGTCGGGCCTCCGGGTCCTGACAGGTTAGTGGCAGTGG  
ATCAGGCACAGATTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT  
GGGGTTTATTACTGCATGCAAACACTACAAACTATCACCTTCGGCCAAGGGGA  
CACGACTGGAGATTAAAC (SEQ ID NO:87)

**D -- Cur2 1.49.1 light chain protein sequence**

DIVMTQSPLSLPVTPGEPAISCRSSQSLHSNGNYLDWYLLKPGQSPQLLIYLG  
SSRASGVPDFRGSGSGTDFTLKISRVEAEDVGYYCMQLQTITFGQGTRLEIK  
(SEQ ID NO:45)



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**FIGURE 20**

**A -- Cur2 1.51 heavy chain nucleotide sequence**

```
GAGGTGCAGCTGGTGCAGTCGGGAGCTGAGGTGAAAAAGCCCGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTCTGGATACAGCTTACCACTGGACTGGATCGG  
CTGGGTGCGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTACTCTGATGCCAATACAGCCCCTCCTCCAAGGCCAGGTACCA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACTATGATTACGTTGGA  
GGAATTATCGGTATACAGGGTGGTCGACCCCTGGGCCAGGGAACCTGGT  
CACCGTCTCCTCAG (SEQ ID NO:88)
```

**B -- Cur2 1.51.1 heavy chain protein sequence**

```
EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDAKYSPSFQGVVTISADKSISTAYLQWSSLKASDTAMYCARHYDYVWRNY  
RYTGWFDPWGQGTLTVSS (SEQ ID NO:46)
```

**C -- Cur2 1.51.1 light chain nucleotide sequence**

```
GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTGTCTCCAGGGGAAAG  
AGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAGCAGCTACTTAGCC  
TGGTACCAAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCAT  
CCAACAGGGCCACTGGCATCCCAGACAGGTTAGTGGCAGTGGGTCTGGGAC  
AGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTCAGTGTATT  
ACTGTCAGCAGTATGGTAGCTCACTATTCACTTCGGCCCTGGGACCAAAGTG  
GATATCAAAC (SEQ ID NO:89)
```

**D -- Cur2 1.51.1 light chain protein sequence**

```
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRA  
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLSFTFGPGTKVDIK (SEQ  
ID NO:47)
```



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**FIGURE 21**

A -- Cur2 6.4 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAACGCTGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCGATTATGATATCAAC  
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATAAAC  
CCTAATAGTGGTAACACAGACTATGCACAGAAAGTTCCAGGGCAGAGTCACCA  
TGACCAGGGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG  
ATCTGAGGACACGGCCATATATTATTGTGTGAGAGGGCTTGGATACAGCTAT  
AATTACGACTACTATTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCA  
CCGTCTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN  
PNSGNTDYAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY  
DYYYGMDVGQGTTTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCGTCTTGTCCTCCAGGGAAAG  
AGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGTAGTTACTTAGCCT  
GGTACCAAGCAGAACGCCTGGCCAGGCTCCCAGGCTCCTCATCTATGCTACATC  
CAGCAGGGCCACTGGCATCCAGACAGGTTAGTGGCAGTGGTCTGGGACA  
GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTCAGTGTATTA  
CTGTCAGCAGTATGGTAGTTACCGTGCAGTTGGCCAGGGGACCAAGCTG  
GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

EIVLTQSPGTLSSLPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRA  
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFQGTLEIK (SEQ  
ID NO:49)



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**FIGURE 22A**

Clone	Germline genes used			No. of Nucleotide/ Amino acid changes							
		V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V				D & J		
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.51.1	VH	S-51	D3-16	JH5B	2/0	0/0	0/0	0/0	1/1	1/1	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0



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**FIGURE 22B**

Clone	Germline genes used			No. of Nucleotide/ Amino acid changes							
		V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V				D & J		
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.51.1	VH	S-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0



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**FIGURE 23**

Figure 23A

						Section 1	
	(1)	1	10	20	30	40	51
CUR2-1.6.1_HC VH3-21	(1)	EVQLVESGGGLVKP <span style="background-color: yellow;">GGG</span> SLRLSCAASGFNFR	SY	NMNMWVRQAPGK <span style="background-color: yellow;">G</span> KGLEWVSS			
	(1)	EVQLVESGGGLVKP <span style="background-color: yellow;">GGG</span> SLRLSCAASGF <span style="background-color: yellow;">T</span> F	S	Y	MNWVRQAPGK <span style="background-color: yellow;">G</span> KGLEWVSS		
	(1)	EVQLVESGGGLVKP <span style="background-color: yellow;">GGG</span> SLRLSCAASGF P SY		MNWVRQAPGK <span style="background-color: yellow;">G</span> KGLEWVSS			
Consensus	(1)	EVQLVESGGGLVKP <span style="background-color: yellow;">GGG</span> SLRLSCAASGF P SY		MNWVRQAPGK <span style="background-color: yellow;">G</span> KGLEWVSS			
						Section 2	
	(52)	52	60	70	80	90	102
CUR2-1.6.1_HC VH3-21	(52)	SSSESSN <span style="background-color: yellow;">I</span> YADSVKGRFTI <span style="background-color: yellow;">S</span> RDN <span style="background-color: yellow;">A</span> NSLYL <span style="background-color: yellow;">I</span> QMN <span style="background-color: yellow;">S</span> LRAEDTAVYYC <span style="background-color: yellow;">R</span>					
	(52)	SSSESSY <span style="background-color: yellow;">I</span> YADSVKGRFTI <span style="background-color: yellow;">S</span> RDN <span style="background-color: yellow;">A</span> NSLYL <span style="background-color: yellow;">I</span> QMN <span style="background-color: yellow;">S</span> LRAEDTAVYYC <span style="background-color: yellow;">R</span>					
	(52)	SSSSSS <span style="background-color: yellow;">I</span> YADSVKGRFTI <span style="background-color: yellow;">S</span> RDN <span style="background-color: yellow;">A</span> NSLYL <span style="background-color: yellow;">I</span> QMN <span style="background-color: yellow;">S</span> LRAEDTAVYYC <span style="background-color: yellow;">R</span>					
Consensus	(52)	SSSSSS <span style="background-color: yellow;">I</span> YADSVKGRFTI <span style="background-color: yellow;">S</span> RDN <span style="background-color: yellow;">A</span> NSLYL <span style="background-color: yellow;">I</span> QMN <span style="background-color: yellow;">S</span> LRAEDTAVYYC <span style="background-color: yellow;">R</span>					
						Section 3	
	(103)	103	110	126			
CUR2-1.6.1_HC VH3-21	(103)	TFGGIIASFYFDYWGQGT <span style="background-color: yellow;">L</span> TVSS					
	(99)	-					
Consensus	(103)	-					

*Figure 23B*



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**FIGURE 24**

**Figure 24A**

	Section 1					
	(1) 1	10	20	30	40	51
Cur2-1.11.1_HC	(1) EVOLVE8GGGLIOPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
VH3-53	(1) EVOLVE8GGGLIOPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
Consensus	(1) EVOLVE8GGGLIOPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
	Section 2					
	(52) 52	60	70	80	90	102
Cur2-1.11.1_HC	(52) Y8GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTN					
VH3-53	(52) Y8GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTN					
Consensus	(52) Y8GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTN					
	Section 3					
	(103) 103	110	120			
Cur2-1.11.1_HC	(103) YYGGMDVWGQGTTTVSS					
VH3-53	(98) -----					
Consensus	(103)					

**Figure 24B**

	Section 1					
	(1) 1	10	20	30	40	51
CUR2-1.11.1_LC	(1) DIVMTQSPLSLPVTPGEPASTISCRASQSLLOSNGYNYLDWYLQKPGQSPLQL					
A19	(1) DIVMTQSPLSLPVTPGEPASTISCRSSQSLLHSNGYNYLDWYLQKPGQSPLQL					
Consensus	(1) DIVMTQSPLSLPVTPGEPASTISCRSSQSLL SNGYNYLDWYLQKPGQSPLQL					
	Section 2					
	(52) 52	60	70	80	90	102
CUR2-1.11.1_LC	(52) LIYLGNSRASGVPDFRGSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF					
A19	(52) LIYLGNSRASGVPDFRGSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF					
Consensus	(52) LIYLGNSRASGVPDFRGSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF					
	Section 3					
	(103) 103	111				
CUR2-1.11.1_LC	(103) GGGTKVEIK					
A19	(101) -----					
Consensus	(103)					



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**FIGURE 25**

**Figure 25A**

	1	10	20	30	40	51	Section 1
CR2-1.17.1 HC	(1)	QVQLVE3GGGVVQPG	BIRLSCAASGFTFSSYGMHWWVRQAPGKGLEWVAVI				
VH3-33	(1)	QVQLVE3GGGVVQPG	BIRLSCAASGFTFSSYGMHWWVRQAPGKGLEWVAVI				
Consensus	(1)	QVQLVE3GGGVVQPG	BIRLSCAASGFTFSSYGMHWWVRQAPGKGLEWVAVI				
	52	60	70	80	90	102	Section 2
CR2-1.17.1 HC	(52)	WYDG8NKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY					
VH3-33	(52)	WYDG8NKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---					
Consensus	(52)	WYDG8NKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR					
	103	110	126				Section 3
CR2-1.17.1 HC	(103)	RYAGYYYYDYGMDVWGQGTTTVSS					
VH3-33	(99)	-----					
Consensus	(103)						

**Figure 25B**

	1	10	20	30	40	52	Section 1
CR2-1.17.1 LC	(1)	DIQMTQSPS8L8ASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA					
A30	(1)	DIQMTQSPS8L8ASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA					
Consensus	(1)	DIQMTQSPS8L8ASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA					
	53	60	70	80	90	104	Section 2
CR2-1.17.1 LC	(53)	S1Q8GVPSRF3GSGSGTEFTLTIS3LQPEDFATYYCLQHN3YPLTFGGGTKV					
A30	(53)	S1Q8GVPSRF3GSGSGTEFTLTIS3LQPEDFATYYCLQHN3YPLTFGGGTKV					
Consensus	(53)	S1Q8GVPSRF3GSGSGTEFTLTIS3LQPEDFATYYCLQHN3YPLTFGGGTKV					
	105	1067					Section 3
CR2-1.17.1 LC	(105)	EIK					
A30	(96)	---					
Consensus	(105)						



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**FIGURE 26**

**Figure 26A**

						Section 1
	(1) 1	10	20	30	40	52
CR2-1.18_HC	(1) QVQLVQSGAEVKRPGAVKVKVSKCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
VH1-8	(1) QVQLVQSGAEVKKPGAVVKVSKCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
Consensus	(1) QVQLVQSGAEVKKPGAVVKVSKCKASGYTFTSYDINWVRQATGQGLEWMGWMN					Section 2
	(53) 53	60	70	80	90	104
CR2-1.18_HC	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELESSLRSEDTAVYYCAR					
VH1-8	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELESSLRSEDTAVYYCAR					
Consensus	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELESSLRSEDTAVYYCAR					Section 3
	(105) 105	110	126			
CR2-1.18_HC	(105) GTYYYYYYYGMDVWGQGTTTVSS					
VH1-8	(99) -----					
Consensus	(105)					

**Figure 26B**

						Section 1
	(1) 1	10	20	30	40	53
CR2-1.18_LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKEGKAKPKRLIYAASS					
A30	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKEGKAKPKRLIYAASS					
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKEGKAKPKRLIYAASS					Section 2
	(54) 54	60	70	80	90	106
CR2-1.18_LC	(54) LQSGVPSRFSGSGSGTEFTLTISLOPEDFATY					
A30	(54) LQSGVPSRFSGSGSGTEFTLTISLOPEDFATY					
Consensus	(54) LQSGVPSRFSGSGSGTEFTLTISLOPEDFATY					Section 3
	(107) MD7					
CR2-1.18_LC	(107) K					
A30	(96) -					
Consensus	(107)					



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**FIGURE 27**

**Figure 27A**

						Section 1
	(1)	10	20	30	40	52
Cur2-1.19.1_hc	(1)	QVOLVQSGAEVKRPGASVKV8CKA8GYTFTSYDINWVRQATGQGLEWMGWMN				
VH1-8	(1)	QVQLVQSGAEVKRPGASVKV8CKA8GYTFTSYDINWVRQATGQGLEWMGWMN				
Consensus	(1)	QVQLVQSGAEVKRPGASVKV8CKA8GYTFTSYDINWVRQATGQGLEWMGWMN				
						Section 2
	(53)	53	60	70	80	90
Cur2-1.19.1_hc	(53)	PNSGNTGYAQKFQGPVTMTRNTSISI8TAYMELSSLRSEDTAVYYCARDVMITF				104
VH1-8	(53)	PNSGNTGYAQKFQGPVTMTRNTSISI8TAYMELSSLRSEDTAVYYCAR-----				
Consensus	(53)	PNSGNTGYAQKFQGPVTMTRNTSISI8TAYMELSSLRSEDTAVYYCAR				
						Section 3
	(105)	105	110	126		
Cur2-1.19.1_hc	(105)	GGVIVHYGMDVWGQGTTTVSS				
VH1-8	(99)	-----				
Consensus	(105)					

**Figure 27B**

						Section 1
	(1)	10	20	30	40	52
Cur2-1.19.1_lc	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRLIYAAS				
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRLIYAAS				
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRLIYAAS				
						Section 2
	(53)	53	60	70	80	90
Cur2-1.19.1_lc	(53)	SIQSGVPSRFSGSGSGTFTLTISSLQPEDFATYYCLQHN3DPCSFQGQTKL				104
A30	(53)	SIQSGVPSRFSGSGSGTFTLTISSLQPEDFATYYCLQHN3YP-----				
Consensus	(53)	SIQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSP				
						Section 3
	(105)	105				
Cur2-1.19.1_lc	(105)	EIR				
A30	(96)	---				
Consensus	(105)					



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**FIGURE 28**

Figure 28A

	Section 1					
	(1)	10	20	30	40	
Cur2-1.23.1_HC VH5-51	(1)	EVQLVQ8GABVKKPGE8LK1SCEGGSGV8FTSYWIGWVREOMP GKGLEWMGII				51
	(1)	EVQLVQ8GABVKKPGE8LK1SCKGSGY8FTSYWIGWVREOMP GKGLEWMGII				
	(1)	EVQLVQ8GAEVKKPGE8LK1SC GSGY8FTSYWIGWVREOMP GKGLEWMGII				
Consensus	(1)	EVQLVQ8GABVKKPGE8LK1SC GSGY8FTSYWIGWVREOMP GKGLEWMGII				
						Section 2
	(52)	52	60	70	80	90
Cur2-1.23.1_HC VH5-51	(52)	YPCGDSDTFYSPSFQGQVTISADKSI	STAYLQWSSLKA	SDTAMYYCARHVSY		102
	(52)	YPCGDSDTRYSPSFQGQVTISADKSI	STAYLQWSSLKA	SDTAMYYCAR-----		
	(52)	YPCGDSDTRYSPSFQGQVTISADKSI	STAYLQWSSLKA	SDTAMYYCAR		
Consensus	(52)	YPCGDSDTRYSPSFQGQVTISADKSI	STAYLQWSSLKA	SDTAMYYCAR		
						Section 3
Cur2-1.23.1_HC VH5-51	(103)	103	110	126		
	(103)	YYV8G8YYNVPDYWGQGTLTVSS				
	(99)	---	---	---		
Consensus	(103)	YYV8G8YYNVPDYWGQGTLTVSS				

Figure 28B

							Section 1
	(1)	10	20	30	40	50	
Cur2-1.23.1_LC A30 Consensus	(1)	DIGMTQSPSSL	SASVGDRVTITCRASQGIRNDLGWYQQ	PGKAPKR	KR	LITYAA	
	(1)	DIGMTQSPSSL	SASVGDRVTITCRASQGIRNDLGWYQQ	PGKAPKR	KR	LITYAA	
	(1)	DIGMTQSPSSL	SASVGDRVTITCRASQGIRNDLGWYQQ	PGKAPKR	KR	LITYAA	
							Section 2
	(52)	60	70	80	90	102	
Cur2-1.23.1_LC A30 Consensus	(52)	SSLQRGVPSRF	SGSGSGTEFTLT	TISSILQPEDFATYYCLQHNSYPWTFQGQT			
	(52)	SSLQRGVPSRF	SGSGSGTEFTLT	TISSILQPEDFATYYCLQHNSYP-----			
	(52)	SSLIQ	GVPFRFSGSGSGTEFTLT	TISSILQPEDFATYYCLQHNSYP			
							Section 3
	(103)	103	107				
Cur2-1.23.1_LC A30 Consensus	(103)	KVEIK					
	(103)	-----					
	(96)	-----					



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**FIGURE 29**

**Figure 29A**

	Section 1					
	(1) 1	10	20	30	40	51
CR2-1.24.1_HC	(1) QVQLVESGGGVVQPGRLSRLSCAASGF		FSSYGMHWVROAEPGKGLEWVA VH3-33			
	(1) QVQLVESGGGVVQPGRLSRLSCAASGF		FSSYGMHWVROAEPGKGLEWVA I			
Consensus	(1) QVQLVESGGGVVQPGRLSRLSCAASGFSFSSYGMHWVROAEPGKGLEWVA					
	Section 2					
	(52) 52	60	70	80	90	102
CR2-1.24.1_HC	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY					
VH3-33	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR					---
Consensus	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR					
	Section 3					
	(103) 103	110	126			
CR2-1.24.1_HC	(103) SYGYVYYDYGMDVWGQGTTVTVSS					
VH3-33	(99) -----					
Consensus	(103)					

**Figure 29B**

	Section 1					
	(1) 1	10	20	30	40	52
CR2-1.24.1_LC	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLLIYAA					
A30	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLLIYAA					
Consensus	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLLIYAA					
	Section 2					
	(53) 53	60	70	80	90	104
CR2-1.24.1_LC	(53) SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNSXPWTFGQGTKV					
A30	(53) SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNSYP					---
Consensus	(53) SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNSYP					
	Section 3					
	(105) 1067					
CR2-1.24.1_LC	(105) EIK					
A30	(96) ---					
Consensus	(105)					



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**FIGURE 30**

**Figure 30A**

						Section 1
VH5-51	(1) 1	10	20	30	40	51
CR2-1.25.1_HC	(1) EVQLVQSGAEVKRPGESLKRISCKGSGYSPSYWIGWVRQMPGKGLEWMGII					
Consensus	(1) EVQLVQSGAEVKKPGESLKRISCKGSGYFTSYWIGWVRQMPGKGLEWMGII					
						Section 2
VH5-51	(52) 52	60	70	80	90	102
CR2-1.25.1_HC	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---					
Consensus	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSY					
						Section 3
VH5-51	(103) 103	110		126		
CR2-1.25.1_HC	(103) YYGSETYYNVFDYWGQGTLTVSS					
Consensus	(103)					

**Figure 30B**

						Section 1
A30	(1) 1	10	20	30	40	52
CR2-1.25.1_LC	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA					
Consensus	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA					
						Section 2
A30	(53) 53	60	70	80	90	104
CR2-1.25.1_LC	(53) SLQSGVPSPFSGSGSGTEFTLTISSLQPEDPATYYCLQHNSYP-----					
Consensus	(53) SLQSGVPSPFSGSGSGTEFTLTISSLQPEDPATYYCLQHNSYPWTFGQGKTV					
						Section 3
A30	(105) 1067					
CR2-1.25.1_LC	(105) EIK					
Consensus	(105)					



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**FIGURE 31**

**Figure 31A**

	(1)	10	20	30	40	52	Section 1
VH5-51	(1) EVQLVQSGAEVKPGESLKIISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIY						
CR2-1.29_HC	(1) EVQLVQSGAEVKPGESLKIISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIY						
Consensus	(1) EVQLVQSGAEVKPGESLKIISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIY						
	(53)	53	60	70	80	90	104
VH5-51	(53) PGDSLTRYSPSFQGOVTISADKSISTAYLQWSSLRASDTAMYCAR-----						
CR2-1.29_HC	(53) PGDSLTRYSPSFQGOATISADKSISTAYLQWSSLRASDTAMYCARHVDUGA						
Consensus	(53) PGDSLTRYSPSFQGOQ TISADKSISTAYLQWSSLRASDTAMYCAR						
	(105)	105	110		129		Section 3
VH5-51	(99) -----						
CR2-1.29_HC	(105) TIGGYYYYYHGMDVWGQGTTVTVSS						
Consensus	(105)						

**Figure 31B**

	(1)	10	20	30	40	53	Section 1
A19	(1) DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLI						
CR2-1.29_LC	(1) DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLI						
Consensus	(1) DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLI						
	(54)	54	60	70	80	90	106
A19	(54) YLGSNRASGVPDFSGSGSGTDFTLKISRVEADVGVYYCMQALQP-----						
CR2-1.29_LC	(54) YLGSNRASGVPDFSGSGSGTDFTLKISRVEADVGVYYCMQALQLMCSFGQ						
Consensus	(54) YLGSNRASGVPDFSGSGSGTDFTLKISRVEADVGVYYCMQALQ						
	(107)	107	113				Section 3
A19	(101) -----						
CR2-1.29_LC	(107) GTKLEIRK						
Consensus	(107)						



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### FIGURE 32

#### Figure 32A

						Section 1
	(1) 1	10	20	30	40	52
VH1-18	(1) QVQLVQSGAEVKKPGASVVKVSCKASGYTFTSYGISMVRQAPGQGLEWMGWIS					
CR2-1.33_HC	(1) QVQLVQSGAEVKKPGASVVKVSCKASGYTFTSYGISMVRQAPGQGLEWMGWIS					
Consensus	(1) QVQLVQSGAEVKKPGASVVKVSCKASGYTFTSYGISMVRQAPGQGLEWMGWIS					
						Section 2
	(53) 53	60	70	80	90	104
VH1-18	(53) AYNGNTNYAQKLOQGRVTMTTDTSSTSTAYMELRSIRSDDTAVYYCAR-----					
CR2-1.33_HC	(53) AYNGNTNYAQKLOQGRVTMTTDTSSTSTAYMELRSIRSDDTAVYYCARDHYDS					
Consensus	(53) AYNGNTNYAQKLOQGRVTMTTDTSSTSTAYMELRSIRSDDTAVYYCAR					
						Section 3
	(105) 105	110	120			
VH1-18	(99) -----					
CR2-1.33_HC	(105) SDYLYYYYYGLDVWGQGTTTVTVSS					
Consensus	(105)					

#### Figure 32B

						Section 1
	(1) 1	10	20	30	40	53
A20	(1) DIQMTQSPSSLSASVGDRVTITCRASQGI SNYLAWYQQKPGKVPKLLIYAAST					
CR2-1.33_LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGI SNYLAWYQQKPGKVPKLLIYAAST					
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGI SNYLAWYQQKPGKVPKLLIYAAST					
						Section 2
	(54) 54	60	70	80	90	106
A20	(54) DQSGVPSRFSGSGSGTDFLTLSISSLQPEDVATYYCQKYN SAP-----					
CR2-1.33_LC	(54) DQSGVPSRFSGSGSGTDFLTLSISSLQPEDVATYYCQKYN SAPLTFGGGTKVEI					
Consensus	(54) DQSGVPSRFSGSGSGTDFLTLSISSLQPEDVATYYCQKYN SAP					
						Section 3
(107) M7						
A20	(96) -					
CR2-1.33_LC	(107) K					
Consensus	(107)					



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**FIGURE 33**

**Figure 33A**

										Section 1	
VH3-33	(1)	1	10	20	30	40	51				Section 2
CR2-1.38.1_HC	(1)	QVQLVEBGGGVVQPGRSIRLSCAASGFTFSSYGMHHWVRQAPGKGLEWVALL									
Consensus	(1)	QVQLVEBGGGVVQPGRSIRLSCAASGFTFSSYGMHHWVRQAPGKGLEWVALL									
										Section 3	
VH3-33	(52)	52	60	70	80	90	102				Section 1
CR2-1.38.1_HC	(52)	WYDGGSNKYYADSVKGRFTI	SRDNNSKNTLYLQMNSLRRAEDTAVYYCAR	---							Section 2
Consensus	(52)	WYDGNDKYYADSVKGRFTI	SRDNNSKNTLYLQMNSLRRAEDTAVYYCAR	GARGYYY							Section 3
VH3-33	(99)	---									Section 1
CR2-1.38.1_HC	(103)	DSSSDYLYYYGMDVWGQGTTVTVSS									Section 2
Consensus	(103)	DSSSDYLYYYGMDVWGQGTTVTVSS									Section 3

**Figure 33B**

										Section 1	
A20	(1)	1	10	20	30	40	52				Section 2
CR2-1.38.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAA									Section 3
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAA									Section 1
A20	(53)	53	60	70	80	90	104				Section 2
CR2-1.38.1_LC	(53)	TLQSGVPSRFSGSGSGTDF	LTISISSLQPEDVAATYYCQKNSAP	---							Section 3
Consensus	(53)	TLQSGVPSRFSGSGSGTDF	LTISISSLQPEDVAAYYCQKCNSAFWTFGQGTTV								Section 1
A20	(96)	---									Section 2
CR2-1.38.1_LC	(105)	EIK									Section 3
Consensus	(105)	EIK									Section 1



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**FIGURE 34**

**Figure 34A**

						Section 1
VH5-51	(1) 1	10	20	30	40	51
CR2-1.39.1_HC	(1) EVOLVQSGAEVKRPGESELKISCKGSGYSPFTSYWIGWVRQMPGKGLEWMGII					
Consensus	(1) EVQLVQSGTEVKRPGESELKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII					
					Section 2	
VH5-51	(52) 52	60	70	80	90	102
CR2-1.39.1_HC	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---					
Consensus	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR				Section 3	
VH5-51	(103) 103	110	126			
CR2-1.39.1_HC	(103) YYNSGSYYNVFDYWGQGTLTVSS					
Consensus	(103)					

**Figure 34B**

						Section 1
A30	(1) 1	10	20	30	40	52
CR2-1.39.1_LC	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKEGKAPKRLIYAA					
Consensus	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKEGKAPKRLIYAA					
					Section 2	
A30	(53) 53	60	70	80	90	104
CR2-1.39.1_LC	(53) SLQSGVPSPRFSGSGSGTEFTLTISSLQPEDPATYYCLQHNSYP-----					
Consensus	(53) SLQSGVPSPRFSGSGSGTEFTLTISSLQPEDPATYYCLQHNSYPWTFGQGTKV				Section 3	
A30	(105) 1087					
CR2-1.39.1_LC	(105) EIK					
Consensus	(105)					



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**FIGURE 35**

**Figure 35A**

	Section 1				
	(1) 1	10	20	30	40
VH1-8	(1) QVQLVQSGAEVKREGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNN				52
CR2-1.45_HC	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNN				
Consensus	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNN				
	Section 2				
	(53) 53	60	70	80	90
VH1-8	(53) PN5GNTGYAQQKPGQGRVTMTRNTSISTAYMELSSLRSED TAVYYCAR-----				104
CR2-1.45_HC	(53) PN5GNTGYAQQKPGQGRVTMTRNTSISTAYMELSSLRSED TAVYYCAR GSGSY				
Consensus	(53) PN5GNTGYAQQKPGQGRVTMTRNTSISTAYMELSSLRSED TAVYYCAR				
	Section 3				
	(105) 105	110	125		
VH1-8	(99) -----				
CR2-1.45_HC	(105) GYDYYYYGMDVWGQGTTTVSS				
Consensus	(105)				

**Figure 35B**

	Section 1				
	(1) 1	10	20	30	40
A20	(1) DIQMTQSPSSLSASVGDRVTITCRASQGINSNYLAWYQQKPGKVPKLLIYAAST				53
CR2-1.45_LC	(1) DIQMTQSPSSLSASVGDRVTINCRA S QG I S N D L A W Y Q Q K P G K V P K L L I Y A A S T				
Consensus	(1) DIQMTQSPSSLSASVGDRVTI CRASQG I S N L A W Y Q Q K P G K V P K L L I Y A A S T				
	Section 2				
	(54) 54	60	70	80	90
A20	(54) DQSGVE3RF3GSG3GTDFLTISLQPEDVATYYCQKYNSAP-----				106
CR2-1.45_LC	(54) DQLGVE3RF3GSG3GTDFLTISLQPEDVATYYCQKYNSAPFTFGPGTKVDI				
Consensus	(54) LQ GVP3RF3GSG3GTDFLTISLQPEDVATYYCQKYNSAP				
	Section 3				
	(107) P07				
A20	(96) -				
CR2-1.45_LC	(107) K				
Consensus	(107)				



3 0 0 4 3 2 6 0 4 0 8 1 3 0 0 2  
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**FIGURE 36**

**Figure 36A**

	(1)	10	20	30	40	51	Section 1
VH1-8	(1) OVQLVOSGAEVKPGASVKVSCKASGY	FTSYDINWVRQATGGLEWMGWM					
CR2-1.46.1_HC	(1) OVQLVOSGAEVKPGASVKVSCKASGY	FTSYDINWVRQATGGLEWMGWM					
Consensus	(1) OVQLVOSGAEVKPGASVKVSCKASGYSFTSYDINWVRQATGGLEWMGWM						
	(52)	52	60	70	80	90	102
VH1-8	(52) NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR	---					
CR2-1.46.1_HC	(52) NPNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARIVV						
Consensus	(52) NPN GNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR						Section 2
	(103)	103	110	126			
VH1-8	(99) -----						
CR2-1.46.1_HC	(103) VVTATDYYYGMDVWGQGTTTVSS						
Consensus	(103)						

**Figure 36B**

	(1)	10	20	30	40	52	Section 1
A30	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLI	I	AAS				
CR2-1.46.1_LC	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLI	I	AAS				
Consensus	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLI	I	AAS				Section 2
	(53)	53	60	70	80	90	104
A30	(53) SLP3GVPSRF3GSG3GTETFTLTISLQPEDFATYYCLQHNSYP	-----					
CR2-1.46.1_LC	(53) SLP3GVPSRF3GSG3GTETFTLTISLQPEDFATYYCLQHSGYPPTFGQGTKV						
Consensus	(53) SL SGVPSRF3GSG3GTETFTLTISLQPEDFATYYCLQH YP						Section 3
	(105)	105	7				
A30	(96) ---						
CR2-1.46.1_LC	(105) EIK						
Consensus	(105)						



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**FIGURE 37**

**Figure 37A**

						Section 1
	(1)	10	20	30	40	51
CR2-1.48.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGTISWVRQAPGQGLEWMGWI				
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGTISWVRQAPGQGLEWMGWI				
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGTISWVRQAPGQGLEWMGWI				
						Section 2
	(52)	52	60	70	80	90
CR2-1.48.1_HC	(52)	SAYNGNTNYAQKLQGRVTMTTDTS	T	STAYMELRSLRSDDTAVYYCARDVEY		102
VH1-18	(52)	SAYNGNTNYAQKLQGRVIMTTDT	S	STAYMELRSLRSDDTAVYYCAR---		
Consensus	(52)	SAYNGNTNYAQKLQGRVTMTTD	S	STAYMELRSLRSDDTAVYYCAR		
						Section 3
	(103)	103	110	125		
CR2-1.48.1_HC	(103)	YYDGSGYYYYFDYWGGTLVTVSS				
VH1-18	(99)	-----				
Consensus	(103)	YYDGSGYYYYFDYWGGTLVTVSS				

**Figure 37B**

						Section 1
	(1)	10	20	30	40	52
CR2-1.48.1_LC	(1)	DIQMTQSPSSSVASVGDRVTITCRASQGIGSSWLAWYQQKEGKAPKLLIYAAS				
L5	(1)	DIQMTQSPSSSVASVGDRVTITCRASQGIGSSWLAWYQQKEGKAPKLLIYAAS				
Consensus	(1)	DIQMTQSPSSSVASVGDRVTITCRASQGIGSSWLAWYQQKEGKAPKLLIYAAS				
						Section 2
	(53)	53	60	70	80	90
CR2-1.48.1_LC	(53)	ILQSGVPSRFSGSGSGTDFTLT	I	SSLQPEDFA	YYCQQNSFPRTFGQGTKV	104
L5	(53)	ILQSGVPSRFSGSGSGTDFTLT	I	SSLQPEDFA	YYCQQNSFP-----	
Consensus	(53)	ILQSGVPSRFSGSGSGTDFTLT	I	SSLQPEDFA	YYCQQNSFP	
						Section 3
	(105)	1087				
CR2-1.48.1_LC	(105)	EIR				
L5	(96)	---				
Consensus	(105)	EIR				



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**FIGURE 38**

**Figure 38A**

	1	10	20	30	40	51	Section 1
CR2-1.49.1_HC	(1)	QVQLVQSGAEVKKGASVVKV3CKA8GYTFTSYDINWVRQATGQGLBWMGWM					
VH1-8	(1)	QVCLVQSGAEVVKKGASVVKV3CKA8GYTFTSYDINWVRQATGQGLBWMGWM					
Consensus	(1)	QVQLVQSGAEVKKGASVVKV3CKA8GYTFTSYDINWVRQATGQGLBWMGWM					Section 2
	52	60	70	80	90	102	
CR2-1.49.1_HC	(52)	NENSGDTGYAOKPQGRVTMTPNTS13TAYMELSSLRSEDTAVYCAR	MRI				
VH1-8	(52)	NENSGNTGYAOKPQGRVTMTPNTS13TAYMELSSLRSEDTAVYCAR	---				
Consensus	(52)	NENSG TGYAOKFQGRVTMTRNTS13TAYMELSSLRSEDTAVYFCAR					Section 3
	103	110	127				
CR2-1.49.1_HC	(103)	VATSYYYYFYGMDVWGQGTTTVSS					
VH1-8	(99)	-----					
Consensus	(103)						

**Figure 38B**

	1	10	20	30	40	51	Section 1
CR2-1.49.1_LC	(1)	DIVMTQSPLSLPVTPGEPAISCR8S0SLLHSNGYNLDWYLLKPGQSPOLL					
A19	(1)	DIVMTQSPLSLPVTPGEPAISCR8S0SLLHSNGYNLDWYLLKPGQSPOLL					
Consensus	(1)	DIVMTQSPLSLPVTPGEPAISCR8S0SLLHSNGYNLDWYLLKPGQSPOLL					Section 2
	53	60	70	80	90	104	
CR2-1.49.1_LC	(53)	IYLG3SRASGVPDFRSGSGSGTDFTLKISRVEAEDVGVYYCMOTIQTITFGQ					
A19	(53)	IYLG3SRASGVPDFRSGSGSGTDFTLKISRVEAEDVGVYYCMOTIQT	---				
Consensus	(53)	IYLG3 RASGVPDFRSGSGSGTDFTLKISRVEAEDVGVYYCMOTIQT					Section 3
	105	111					
CR2-1.49.1_LC	(105)	GTRLEIK					
A19	(101)	-----					
Consensus	(105)						



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**FIGURE 39**

**Figure 39A**

						Section 1
	(1) 1	10	20	30	40	51
CR2-1.51.1_HC	(1) EVOLVQSGAEVKRPGESLKI <b>SCKGSGYSFTSYWIGWVRQMPGKGLEWMGII</b>					
VH5-51	(1) EVQLVQSGAEVKRPGESLKI <b>SCKGSGYSFTSYWIGWVRQMPGKGLEWMGII</b>					
Consensus	(1) EVQLVQSGAEVKRPGESLKI <b>SCKGSGYSFTSYWIGWVRQMPGKGLEWMGII</b>					
						Section 2
	(52) 52	60	70	80	90	102
CR2-1.51.1_HC	(52) YPGDSDA <b>KYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHYDY</b>					
VH5-51	(52) YPGDSDT <b>KYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---</b>					
Consensus	(52) YPGDSD <b>KYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR</b>					
						Section 3
	(103) 103	110	120			
CR2-1.51.1_HC	(103) VWRNYRYTGWFDPWGQGTLVTVSS					
VH5-51	(99) -----					
Consensus	(103)					

**Figure 39B**

						Section 1
	(1) 1	10	20	30	40	52
CR2-1.51.1_LC	(1) EIVLTQSPGTLSLSPGERATLSCRABOSVSSSYLAWYQQKPGQAPRLLIYGA					
A27	(1) EIVLTQSPGTLSLSPGERATLSCRABOSVSSSYLAWYQQKPGQAPRLLIYGA					
Consensus	(1) EIVLTQSPGTLSLSPGERATLSCRABOSVSSSYLAWYQQKPGQAPRLLIYGA					
						Section 2
	(53) 53	60	70	80	90	104
CR2-1.51.1_LC	(53) S <b>NRATGIPDRFSGSGSGTILTTLTISRLEPEDFAVYYCQQYGSSLFTP</b> PGTK					
A27	(53) S <b>SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP</b> -----					
Consensus	(53) S <b>RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS</b>					
						Section 3
	(105) 10508					
CR2-1.51.1_LC	(105) VDIK					
A27	(97) -----					
Consensus	(105)					



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**FIGURE 40**

**Figure 40A**

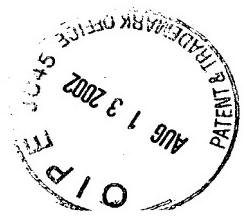
	(1) 1	10	20	30	40	52	Section 1
Cur2-6.4.1 hc	(1) QVQLVQSGAEVKKEGASVVKVSCKA9GYTFTSYDINWUROATGQGLEWMGW						
VH1-8	(1) QVQLVQSGAEVKKEGASVVKVSCKA9GYTFTSYDINWUROATGQGLEWMGW						
Consensus	(1) QVQLVQSGAEVKKGASVVKVSCKA9GYTFTSYDINWUROATGQGLEWMGW						
	(53) 53	60	70	80	90	104	Section 2
Cur2-6.4.1 hc	(53) PNSGNTDYAQKFQGRVTMTRDT SISTAYMELSSRLSED TAIYYCVRGFGY						
VH1-8	(53) PNSGNTGYAQKFQGRVTMTRNT SISTAYMELSSRLSED TAIYYCAR						
Consensus	(53) PNSGNT YAQKFQGRVTMTR TSISTAYMELSSRLSED TAIYYC R						
	(105) 105	110	125				Section 3
Cur2-6.4.1 hc	(105) NYDYYYYGMDVWGQGTTTVSS						
VH1-8	(99) -----						
Consensus	(105)						

**Figure 40B**

	(1) 1	10	20	30	40	52	Section 1
Cur2-6.4.1 Lc	(1) EIVLTQSPGTLSLSPGERATLSRASQEVSSSYLAWYQQKPGQAPRLLIYT						
A27	(1) EIVLTQSPGTLSLSPGERATLSRASQEVSSSYLAWYQQKPGQAPRLLIYA						
Consensus	(1) EIVLTQSPGTLSLSPGERATLSRASQEVSSSYLAWYQQKPGQAPRLLIYA						
	(53) 53	60	70	80	90	104	Section 2
Cur2-6.4.1 Lc	(53) SSRATGIPDRFSGSGSGTDFTLTISRLPELFAYYYCQQYGS SP						
A27	(53) SSRATGIPDRFSGSGSGTDFTLTISRLPELFAYYYCQQYGS SP						
Consensus	(53) SSRATGIPDRFSGSGSGTDFTLTISRLPELFAYYYCQQYGS SP						
	(105) 10508						Section 3
Cur2-6.4.1 Lc	(105) LEIK						
A27	(97) ---						
Consensus	(105)						

CLONE #	VH	#DR	VH END L	# N's Sequence	DH	Size of D	D Sequence	# N's Sequence	JH	# del	JH segment
1.19. 1	DP-15/1- 8	-1	CGAGAG (SEQ ID NO:92)	3 ACG	D3-16	28	TTATGATTACGTT GGGGGAGTTATCGT (SEQ ID NO:93)	2 GC	JH6	-12	ACTACG (SEQ ID NO:94)
1.19. 2	DP-15/1- 8	-1	CGAGAG (SEQ ID NO:92)	3 ACG	D3-16	28	TTATGATTACGTT GGGGGAGTTATCGT (SEQ ID NO:93)	2 GC	JH6	-12	ACTACG (SEQ ID NO:94)
1.19. 3	DP-15/1- 8	-1	CGAGAG (SEQ ID NO:92)	3 ACG	D3-16	28	TTATGATTACGTT GGGGGAGTTATCGT (SEQ ID NO:93)	2 GC	JH6	-12	ACTACG (SEQ ID NO:94)
6.4.1	DP-15/1- 8	0	GAGAGG (SEQ ID NO:95)	3 CTT	D5-18	12	TGGTACAGCTA (SEQ ID NO:96)	2 TA	JH6	0	ATTACTAC (SEQ ID NO:97)
6.4.2	DP-15/1- 8	0	GAGAGG (SEQ ID NO:95)	3 CTT	D5-18	12	TGGTACAGCTA (SEQ ID NO:96)	2 TA	JH6	0	ATTACTAC (SEQ ID NO:97)
6.4.3	DP-15/1- 8	0	GAGAGG (SEQ ID NO:95)	3 CTT	D5-18	12	TGGTACAGCTA (SEQ ID NO:96)	2 TA	JH6	0	ATTACTAC (SEQ ID NO:97)
CLONE	VK	#de	Vk end	#n	N SEQ	n	JK	# del	JK end		
1.19. 1	A3.0	-3	TTACCC (SEQ ID NO:98)	6	GTGCA	JK2	-7	TTTGG (SEQ ID NO:100)			
1.19. 2	A3.0	-3	TTACCC (SEQ ID NO:98)	6	GTGCA	JK2	-7	TTTGG (SEQ ID NO:100)			

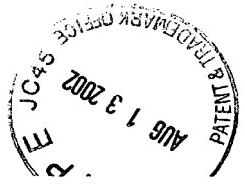
Figure 41A



1.19. 3	A230	-3	TTCACCC (SEQ ID NO:98)	6	GTGCAAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
6.4.1	A27/A27A	-3	CTGACC (SEQ ID NO:101)	6	GTGCAAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)
6.4.2	A27/A27A	-3	CTGACC (SEQ ID NO:101)	6	GTGCAAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)
6.4.3	A27/A27A	-3	CTGACC (SEQ ID NO:101)	6	GTGCAAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)

Figure 41B

ANTIPODIES DIRECTED TO PDGF AND USES THEREOF  
Appl. No.: 10/041,860 Atty. Doctor: ABGENIX,051A  
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CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH segment
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CCTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CCTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGA (SEQ ID NO:105)	14	ATTATGCC TCGTT (SEQ ID NO:106)	JH4B	-1.	CCTACTT (SEQ ID NO:107)
1.11.1	DP-42/3-53	-5	AGAGAG (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	CGGAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.11.2	DP-42/3-53	-5	AGAGAG (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	CGGAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.23.1	DP-73/5-51	0	GAGAGA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	D3-10	19	TTCGGGGAGGTA TTATAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGAA (SEQ ID NO:115)
1.23.2	DP-73/5-51	0	GAGAGA (SEQ ID NO:112)	18	TGTATCGTATTACT ATGT (SEQ ID NO:113)	D3-10	19	TTCGGGGAGGTA TTATAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGAA (SEQ ID NO:115)

Figure 42A



Figure 42B

				#n			
1.6.1	A30	-3	TTACCC	0	0	JK4	0
		(SEQ ID NO:116)					GCTCACT (SEQ ID NO:117)
1.6.2	A30	-3	TTACCC	0	0	JK4	0
		(SEQ ID NO:116)					GCTCACT (SEQ ID NO:117)
1.6.3	A30	-3	TTACCC	0	0	JK4	0
		(SEQ ID NO:116)					GCTCACT (SEQ ID NO:117)
1.11.1	A3/A19/DPK	-4	AAACTC	0	0	JK4	-2
		(SEQ ID NO:118)					TGACTTTC (SEQ ID NO:119)
1.11.2	A3/A19/DPK	-4	AAACTC	0	0	JK4	-2
		(SEQ ID NO:118)					TGACTTTC (SEQ ID NO:119)
1.23.1	A30	-3	TTACCC	0	0	JK1	0
		(SEQ ID NO:120)					GTGGAC (SEQ ID NO:120)
1.23.2	A30	-3	TTACCC	0	0	JK1	0
		(SEQ ID NO:120)					GTGGAC (SEQ ID NO:120)

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Clone #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.17.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:111)	4	TCAA	D5-18	6	GGATACA (SEQ ID NO:122)	9	ATATGCTG (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:111)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.3	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.18	DP-15/1-8	1	CGAGAG (SEQ ID NO:125)	1	A	D8-19	19	GGGTATA CAGTGGCT (SEQ ID NO:126)	4	GACA	JH6B	-2	TACTAC (SEQ ID NO:127)
1.24.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.24.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.26.1	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC	D3-10	30	GTATATT TGGTTCGG AGACTTATT ATAA	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:135)

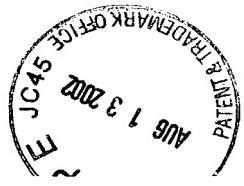
Figure 43A

ANTIBODIES DIRECTED TO PDGF AND USES THEREOF  
Corralan et al.  
Appl. No.: 10/041,860 Atty Doc#: ABGENIX.051A



Clone #	VH	#DEL	VH END	#Ns	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
1.25.2	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTAATTAA TGTTTCGG AGACTTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	-4	CTTGA (SEQ ID NO:134)
1.29	DP-73/5-51	0	GAGACA (SEQ ID NO:135)	1	C	D5-12	21	GTTGATGT AGGGGCT ACGATT (SEQ ID NO:136)	7	GGGGAT	JH6B	0	ATTACTAC (SEQ ID NO:138)
1.33	DP-14/1-18	0	GAGAGA (SEQ ID NO:139)	2	TC	D21-9	18	ATTACTAT GATAGTAG TG (SEQ ID NO:140)	7	ATTATCT (SEQ ID NO:141)	JH6B	-4	CTACTA (SEQ ID NO:142)
1.38.1	DP-50/3-33	1	CGAGAG (SEQ ID NO:143)	2	GA	D21-9	19	TATTACTA TGATAGTA GTG (SEQ ID NO:144)	7	ATTATCT (SEQ ID NO:145)	JH6B	-4	CTACTA (SEQ ID NO:146)
1.39.1	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT AtaaTTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTGA (SEQ ID NO:150)
1.39.2	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT AtaaTTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTGA (SEQ ID NO:150)

Figure 43B



CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
1.40.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.40.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.45	DP-15/1-8	0	GAGAGG (SEQ ID NO:154)	2	CA	DK4	20	GTGGATAAC AGCTATGG TTAC (SEQ ID NO:155)	1	G	JH6B	-6	ACTACT (SEQ ID NO:156)
1.46.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GT GCTGGTA GCTGCTAC (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.46.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.48.1	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATGTTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)
1.48.2	DP-14/1-18	1	CGAGAG	7	TGTTGAA	D21-9	20	TATTACTA	1	T	JH4B	0	ACTACT

Figure 43C

ANTIBODIES DIRECTED TO PDGF AND USES THEREOF  
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 Covdalan et al.



CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
			(SEQ ID NO:160)	(SEQ ID NO:161)				TGATGGTA (SEQ ID NO:162)					(SEQ ID NO:163)
1.49.1	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.49.2	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.51.1	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTTGGG GGAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-6	TGGTC (SEQ ID NO:171)
1.51.2	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTTGGG GGAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-6	TGGTC (SEQ ID NO:171)

Figure 43D

CLONE	VK	#del	Vk end	#n	N SEQ	Jk	#del	Jk end
1.17.1	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)



CLONE	V <sub>K</sub>	#del	V <sub>K</sub> end	#n	N SEQ	J <sub>K</sub>	#del	J <sub>K</sub> end
1.17.2	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.3	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.18	A30	3	TTACCC (SEQ ID NO:174)	0	0	JK3	0	ATTCAC (SEQ ID NO:175)
1.24.1	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.24.2	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.26.1	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.25.2	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.29	A3/A19/DPK	7	CTACAA (SEQ ID NO:180)	14	TCTCTCATG TGCGAG (SEQ ID NO:181)	JK2	7	TTTGG (SEQ ID NO:182)
1.33	A20/DPK4	3	TGCCCC (SEQ ID NO:183)	0	0	JK4	0	GCTCAC (SEQ ID NO:184)
1.38.1	A20/DPK4	3	TGCCCC (SEQ ID NO:185)	0	0	JK1	0	GTGGAC (SEQ ID NO:186)
1.38.1	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)

Figure 43E

ANTIBODIES DIRECTED TO PDGF AND USES THEREOF  
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CLONE	VK	#del	VK end	#n	N SEQ	JK	# del	JK end
1.39.2	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)
1.45	A20/DPK4	3	TGCCCC (SEQ ID NO:189)	0	0	JK3	0	ATTCAC (SEQ ID NO:190)
1.46.1	A30	0	CCCTCC (SEQ ID NO:191)	0	0	JK1	-3	GACGTT (SEQ ID NO:192)
1.46.2	A30	0	CCCTCC (SEQ ID NO:191)	0	0	JK1	-3	GACGTT (SEQ ID NO:192)
1.48.1	L5/DPK5V	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.48.2	L5/DPK5V	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.49.1	A3/A19/DPK	5	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.49.2	A3/A19/DPK	5	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)

Figure 43F

ANTIBODIES DIRECTED TO PGDF AND USES THEREOF  
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Appl. No.: 10/041,860 Atty. Docket: ABGENIX/OSIA

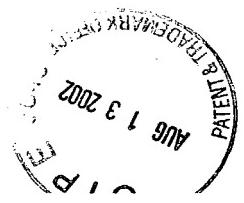
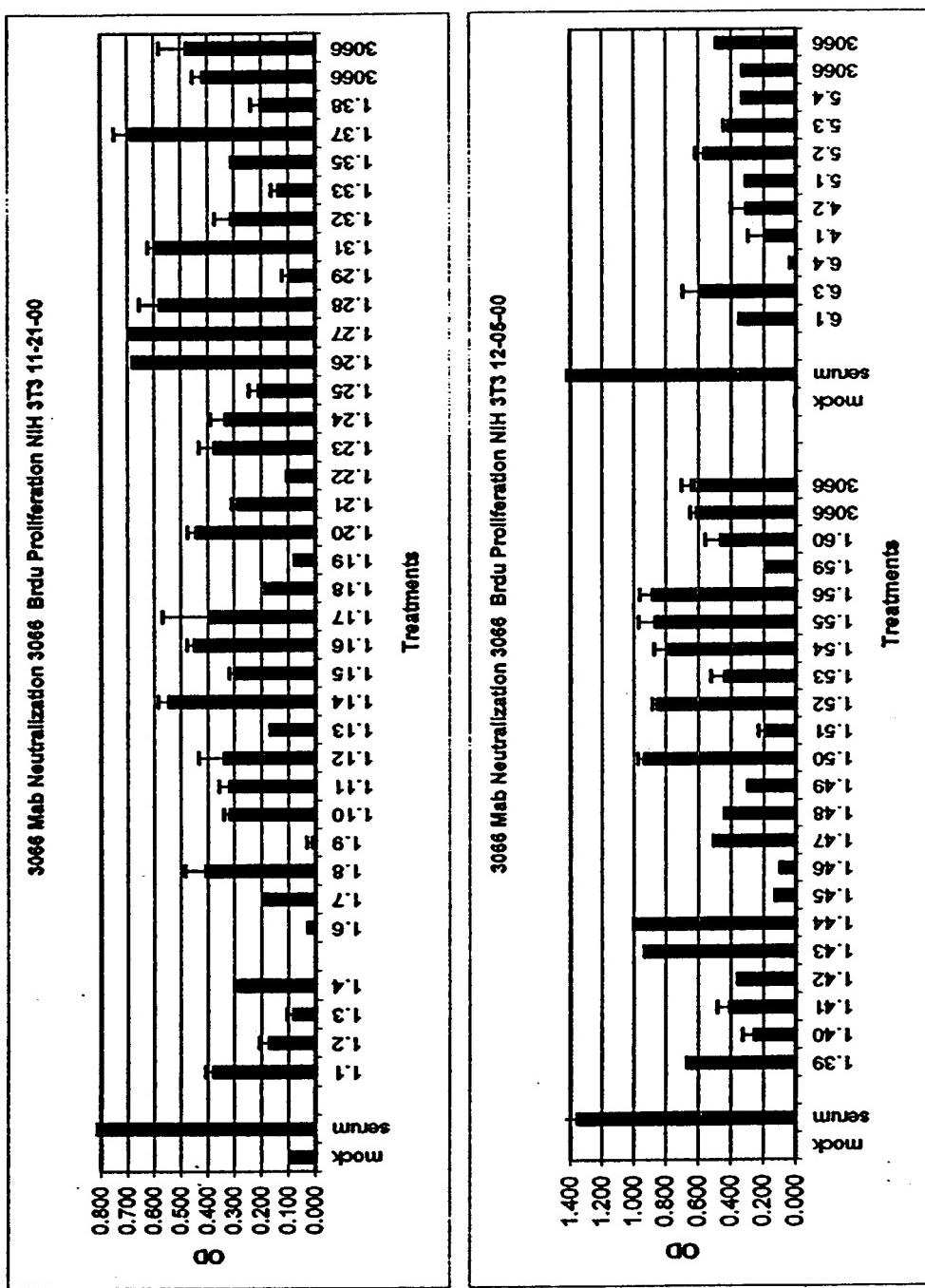


FIGURE 44



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ANTIBODIES DIRECTED TO PDGF AND USES THEREOF

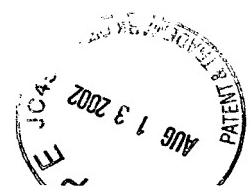
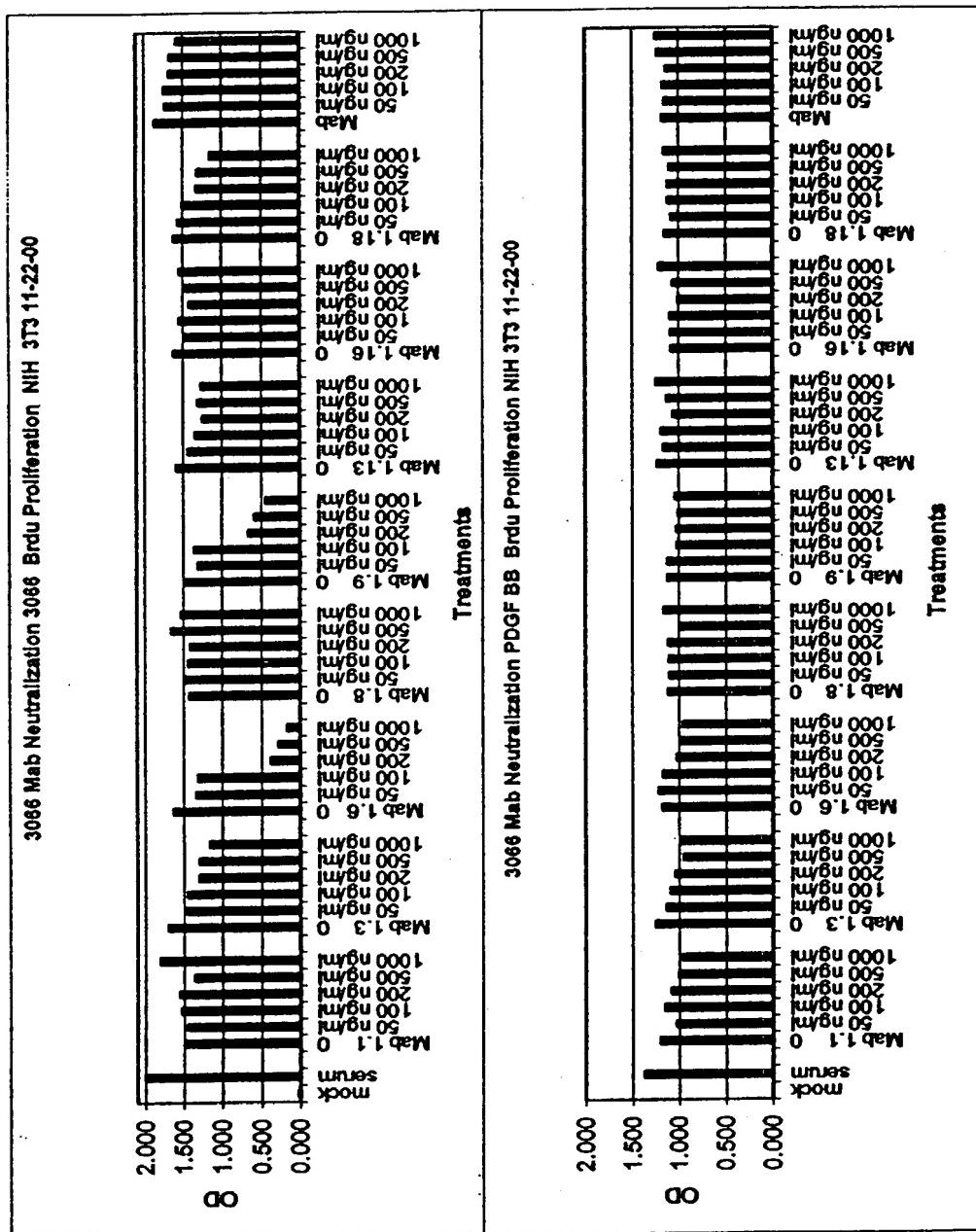


FIGURE 45



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ANTIBODIES DIRECTED TO PDGF AND USES THEREOF

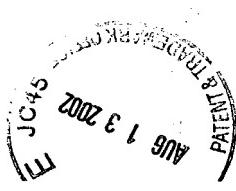
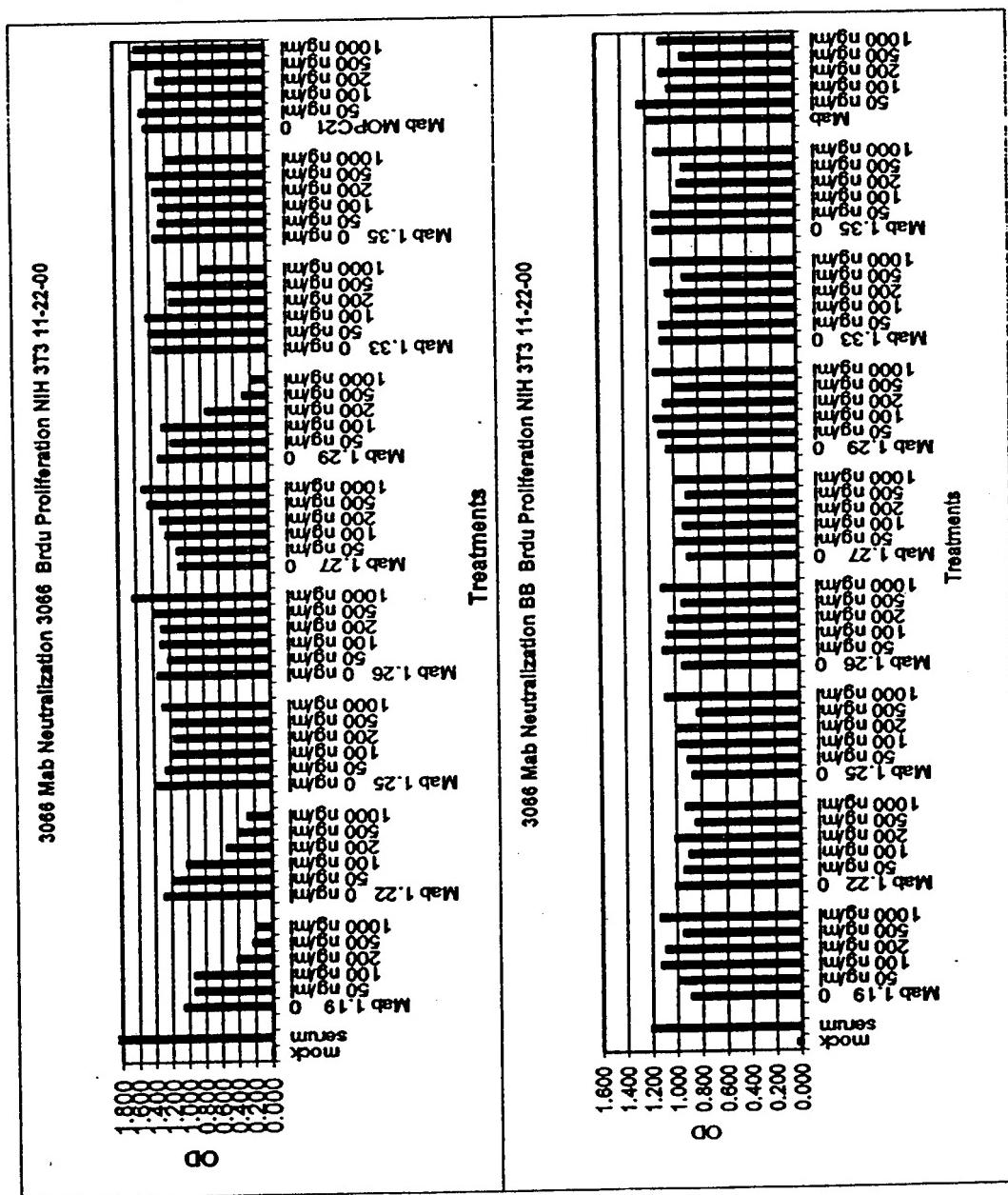


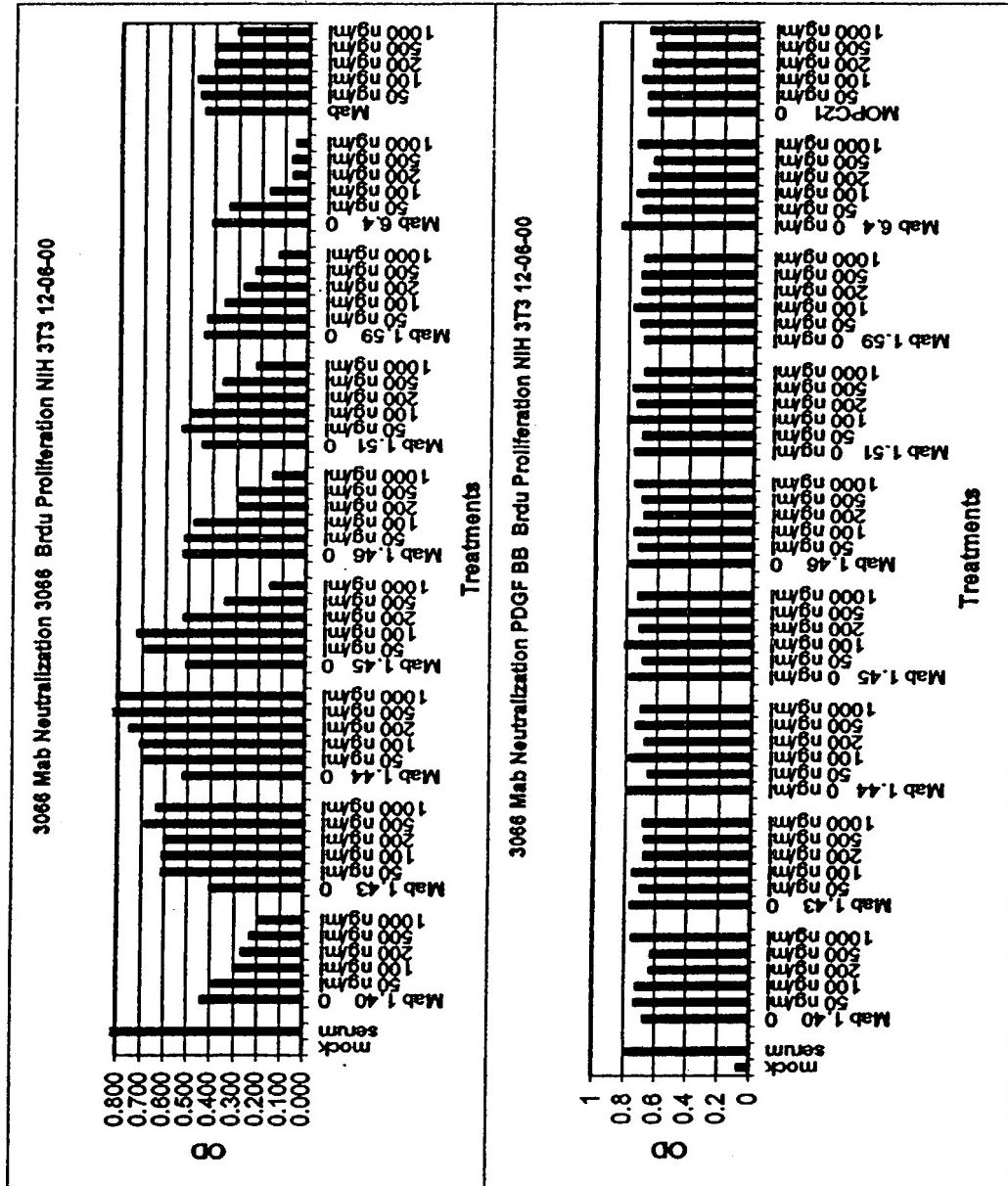
FIGURE 46



ANTIBODIES DIRECTED TO PDGF AND USES THEREOF  
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FIGURE 47



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ANTIBODIES DIRECTED TO PDGF AND USES THEREOF



## ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF

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PATENT

AUG 13 2002

FIGURE 48

1.19 H	1	Q	A	A V V	K	T	D N	T Q	WMNPNSGN G	60	
6.4 H	1	Q	A	A V V	K	T	D N	T Q	WINPNSGN D	60	
1.18 H	1	Q	A	A V V	K	T	D N	T Q	WMNPNSGN G	60	
1.40 H	1	Q	A	A V V	K	T	T D N	T Q	WMNPNSGN G	60	
1.45 H	1	Q	A	A V V	K	T	D N	T Q	WMNPNSGN G	60	
1.46 H	1	Q	A	A V V	K	S	D N	T Q	WMNPNNGN G	60	
1.49 H	1	Q	A	A V V	K	T	D N	T Q	WMNPNSGD G	60	
1.33 H	1	Q	A	A V V	K	T	G S	P Q	WISAYNGN N	60	
1.48 H	1	Q	A	A V V	K	T	G S	P Q	WISAYNGN N	60	
1.6 H	1	E	E	GGLV	G LRL	A	FN RT	NMN	P K	VSSISSSSNIY	60
1.17 H	1	Q	E	GG VQ	K LRL	A	FT S	GMH	P K	VAVIWYDGNSNKY	60
1.24 H	1	Q	E	GG VQ	R LRL	A	FS S	GMH	P K	VADIWYDGNSNKY	60
1.38 H	1	Q	E	GG VQ	R LRL	A	FT S	GMH	P K	VAIIWYDGNDKY	60
1.11 H	1	E	GGLIQ	G LRL	A	FTVS	NYMS	P K	VSVIYSGGS- Y	59	
1.23 H	1	E	A	E L I	EG	S	W G	MP K	IIYPGDSD R	60	
1.25 H	1	E	A	E L I	KG	R	W G	MP K	IIYPGDSD R	60	
1.29 H	1	E	A	E L I	KG	S	W G	MP K	IIYPGDSD R	60	
1.39 H	1	E	T	E L I	KG	R	W G	MP K	IIYPGDSD R	60	
1.51 H	1	E	A	E L I	KG	S	W G	MP K	IIYPGDSDAK	60	
							[ CDR1 ]		[ CDR2 ]		

1.19 H	61	QKF	V MTRNT	I	MELS	SE	V	--DVM-ITFGGVIVH-YGM V	116
6.4 H	61	QKF	V MTRDT	I	MELS	SE	I V	--GFG-YSYN-YD -YGM V	115
1.18 H	61	QKF	V MTRNT	I	MELS	SE	V	--EG--IAVAGTY YYGM V	116
1.40 H	61	QKF	V MTRNT	L	MELS	SE	V	--DIV-VVVAATN -NGM V	116
1.45 H	61	QKF	V MTRNT	I	MELS	SE	V	--GSG-YSYG-YD -YGM V	115
1.46 H	61	QKF	V MTRNT	I	MELS	SE	V	--DIV-VVVTATD -YGM V	116
1.49 H	61	QKF	V MTRNT	I	MELS	SE	V F	--MRD-IVATSYY FYGM V	117
1.33 H	61	QKL	V MTTDT	T	MELR	SD	V	--DHY-YDSSDYL YYGL V	117
1.48 H	61	QKL	V MTTDT	T	MELR	SD	V	DVEYY-YDGSGYY FDY----	115
1.6 H	61	DSVK	F ISRDNAKNSL	LQMN	AE	V	DIMI---TGF-GIIASFYF Y	116	
1.17 H	61	DSVK	F ISRDN KN L	LQMN	AE	V	DQGY---RYA-GY DYGM V	116	
1.24 H	61	DSVK	F ISRDN KN L	LQMN	AE	V	DQGY---SYG-YV DYGM V	116	
1.38 H	61	DSVK	F VSRDN KN L	LQMN	AE	V	GYYYD--SSD-YL YYGM V	117	
1.11 H	60	DSVK	F ISRDN KN L	LQMN	AE	V	GTVTT-----N YYGM V	110	
1.23 H	61	SPSF	QV ISADK I	LQWS	KAS	M	HVSY---YYVSGS -NVF Y	116	
1.25 H	61	SPSF	QV ISADK I	LQWS	KAS	M	HGSY---YYGSET -NVF Y	116	
1.29 H	61	SPSF	QA ISADK I	LQWS	KAS	M	HVDVGATIGGYYY -HGM V	119	
1.39 H	61	SPSF	QV ISADK I	LQWS	KAS	M	HGSY---YYNSGS -NVF Y	116	
1.51 H	61	SPSF	QV ISADK I	LQWS	KAS	M	HYDY---VWRNYR T-GWF P	116	
							[ CDR3 ]		



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FIGURE 48 (CONT)

1.19 H	117	T	126
6.4 H	116	T	125
1.18 H	117	T	126
1.40 H	117	T	126
1.45 H	116	T	125
1.46 H	117	T	126
1.49 H	118	T	127
1.33 H	118	T	127
1.48 H	116	L	125
1.6 H	117	L	126
1.17 H	117	T	126
1.24 H	117	T	126
1.38 H	118	T	127
1.11 H	111	T	120
1.23 H	117	L	126
1.25 H	117	L	126
1.29 H	120	T	129
1.39 H	117	L	126
1.51 H	117	L	126



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FIGURE 49

1.48 L 1	V	T	SS-----W A	A KL	I Q 55
1.49 L 1	L PVTP EPAS S	S SLLHSNGYNY D LL	QS QL	LG SRA 60	
1.11 L 1	L PVTP EPAS S	S SLLQSNGYNY D L	QS QL	LG NRA 60	
1.29 L 1	L PVTP EPAS S	S SLLHSNGYNY D L	QS QL	LG NRA 60	
1.45 L 1	N	SN-----D A	V KL	T Q 55	
1.33 L 1	T	SN-----Y A	V KL	T Q 55	
1.38 L 1	T	SN-----Y A	V NL	T Q 55	
6.4 L 1	E VL GT L P E A LS	SVSSS----Y A	QA RL	T SRA 56	
1.51 L 1	E VL GT L P E A LS	SVSSS----Y A	QA RL	G NRA 56	
1.19 L 1	T	RN-----D G	A KR	S Q 55	
1.18 L 1	T	RN-----D G	A KR	S Q 55	
1.16 L 1	T	RN-----D G F	A KR	S Q 55	
1.23 L 1	T	RN-----D G I	A KR	S Q 55	
1.25 L 1	T	RN-----D G	A KR	S Q 55	
1.39 L 1	T	RN-----D G	A KR	S Q 55	
1.17 L 1	T	RN-----D G	A KR	S Q 55	
1.24 L 1	T	RN-----D G	A KR	S Q 55	
1.46 L 1	T	RN-----D G	A KR	F S P 55	
		[ CDR1 ]		[ CDR2 ]	

1.48 L 56	D	F S	Q SN F R -	Q	107
1.49 L 61	D	K RVEA VGV	M TLQTIT--	Q RL	111
1.11 L 61	D	K RVEA VGV	M ALQTLT--	G	111
1.29 L 61	D	K RVEAD VGV	M ALQSLMCS	Q L	113
1.45 L 56	L	D	V T QKYN A F -	P D	107
1.33 L 56	D	D	V T QKYN A L -	G	107
1.38 L 56	D S	V A QKCN A W -	Q T	107	
6.4 L 57	T I D	D R E F V	Q YG S CS-	Q L	108
1.51 L 57	T I D	D R E F V	Q YG SLF -	P D	108
1.19 L 56	D	F T L HN D CS-	Q L R	107	
1.18 L 56	E	F T F L HN Y F -	P D	107	
1.16 L 56	E	F T L HN Y L -	G	107	
1.23 L 56	R	E	F T L HN Y W -	Q	107
1.25 L 56	E	F T L HN Y W -	Q	107	
1.39 L 56	E	F T L HN Y W -	Q	107	
1.17 L 56	E	F T L HN Y L -	G	107	
1.24 L 56	E	F T L HN Y W -	Q	107	
1.46 L 56	E	F T L HSGY P -	Q	107	
		[ CDR3 ]			



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FIGURE 50

1.19 H 1			I	D	60
6.4 H 1					60
1.18 H 1					60
1.40 H 1		T			60
1.45 H 1					60
1.46 H 1	S		N		60
1.49 H 1			D		60
	[ CDR1 ]		[ CDR2 ]		

1.19 H 61		D	I	V	DVMITFGG-VIVH	119
6.4 H 61				GFGYSYN--YD	118	
1.18 H 61		L		EGIAVAGT-YY	119	
1.40 H 61				DIVVVVAA-TN N	119	
1.45 H 61				GSGYSYG--YD	118	
1.46 H 61			F	DIVVVVTA-TD	119	
1.49 H 61				MRDIVATSYYY F	120	
	[ CDR3 ]					

1.19 H 120	126
6.4 H 119	125
1.18 H 120	126
1.40 H 120	126
1.45 H 119	125
1.46 H 120	126
1.49 H 121	127



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FIGURE 511.33 H 1  
1.48 H 160  
60

[ CDR1 ]

[ CDR2 ]

1.33 H 61  
1.48 H 61--DH S D L YY GLDV 118  
DVEY G G Y FD ---- 116  
[ CDR3 ]

\_\_\_\_\_]

1.33 H 119 T 127  
1.48 H 117 L 125



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FIGURE 52

1.17 H 1	K	T	V	SN	60
1.24 H 1	R	S	D	SN	60
1.38 H 1	R	T	I	ND	60
		[ CDR1 ]		[ CDR2 ]	
1.17 H 61	I		DQG -RYAGY	D	119
1.24 H 61	I		DQG -SYGYV	D	119
1.38 H 61	V		GYY DSSDYL	Y	120
			[ CDR3 ]		
1.17 H 120		126			
1.24 H 120		126			
1.38 H 121		127			



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FIGURE 53

1.23 H 1  
1.25 H 1  
1.29 H 1  
1.39 H 1  
1.51 H 1

T

E	S	60
	R	60
	S	60
	R	60
	S	AK 60

[ CDR1 ] [ CDR2 ]

1.23 H 61  
1.25 H 61  
1.29 H 61  
1.39 H 61  
1.51 H 61

A

\_\_\_\_\_]

VS YYVSG---S	NV	Y	117
GS YYGSE---T	NV	Y	117
VDVGATIGGYYY	HGM	V	120
GS YYNSG---S	NV	Y	117
YD VWRNY---R	TGW	P	117

[ CDR3 ]

1.23 H 118  
1.25 H 118  
1.29 H 121 T 129  
1.39 H 118  
1.51 H 118

126

126

126

126

126



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FIGURE 54

1.49 L 1  
1.11 L 1  
1.29 L 1

H	L	S	60
Q	Q	N	60
H	Q	N	60
[ CDR1 ]		[ CDR2 ]	

1.49 L 61  
1.11 L 61  
1.29 L 61

]

E	T	TIT--	Q	RL	111
E	A	TLT--	G	KV	111
D	A	SLMCS	Q	KL	113
[ CDR3 ]					



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FIGURE 55

1.45 L 1	N	D	K	L	60
1.33 L 1	T	Y	K	S	60
1.38 L 1	T	Y	N	S	60

[ CDR1 ]

[ CDR2 ]

1.45 L 61	T	T	F	P	K	D	107	
1.33 L 61	T	Y	L	G	K	E	107	
1.38 L 61	S	A	C	W	Q	T	E	107

[ CDR3 ]



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FIGURE 56

6.4 L 1  
1.51 L 1

[ CDR1 ]

AT S 60  
GA N 60  
[ CDR2 ]

6.4 L 61  
1.51 L 61

PCS Q LE 108  
LFT P VD 108  
[ CDR3 ]



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FIGURE 57

1.19 L 1								60
1.18 L 1								60
1.16 L 1								60
1.23 L 1			F		I		R	60
1.25 L 1								60
1.39 L 1								60
1.17 L 1								60
1.24 L 1								60
1.46 L 1						F	P	60
				[ CDR1 ]			[ CDR2 ]	
1.19 L 61	D		D	CS	Q	L	R	107
1.18 L 61		F		F	P	D		107
1.16 L 61				L	G			107
1.23 L 61				W	Q			107
1.25 L 61				W	Q			107
1.39 L 61				W	Q			107
1.17 L 61				L	G			107
1.24 L 61				W	Q			107
1.46 L 61				SG	P	Q		107
				[ CDR3 ]				